

STIC-Biotech/ChemLib

CRFE

157528

mej

From: Whiteman, Brian  
Sent: Monday, June 27, 2005 8:06 AM  
To: STIC-Biotech/ChemLib  
Subject: sequence search

10/057,136 Schlom et al. EFD 1/25/02

SEQ ID NOs: 1, 2 and 4-12

- 1) oligonucleotide search against interference databases
- 2) oligonucleotide search against public databases

Thank you,

Brian Whiteman  
Remsen, 2D14  
mail box 2C18  
Patent Examiner - Art Unit 1635  
United States Patent and Trademark Office  
(571) 272-0764

1 aa 20

2 na 60

4

5

6

7

8

9

10

11

12

1  
60

RECEIVED  
JUN 27 2005  
STIC

mej

\*\*\*\*\*  
STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2-\_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*  
Type of Search

NA#: \_\_\_\_\_ AA#: \_\_\_\_\_  
Interference: \_\_\_\_\_ SPDI: \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure#: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*  
Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 29, 2005, 23:23:45 ; Search time 230.7 Seconds  
(without alignments)  
1625.622 Million cell updates/sec

Title: US-10-057-136-4  
Perfect score: 60  
Sequence: 1 ggcagtactgcaccaccggc.....ctgatacaagacgtgcacct 60

Scoring table: OLIGO NUC  
Gapop 60.0, Gapext 60.0

Searched: 6067389 seqs, 3125258755 residues

Word size : 0

Total number of hits satisfying chosen parameters: 12134778

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:  
9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:  
13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:  
14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:  
15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:  
16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:  
17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:  
18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:  
19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq:  
20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq:  
21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq:  
22: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:  
23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq:  
24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:  
25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:  
26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	60	100.0	60	14	US-10-057-136-4
2	60	100.0	2297	17	US-10-406-317-41
3	17	28.3	746	18	US-10-424-599-119193
4	17	28.3	863	18	US-10-424-599-131807
5	17	28.3	891	17	US-10-282-122A-37454
6	17	28.3	1756	17	US-10-282-122A-23378
7	17	28.3	1768	17	US-10-282-122A-19753
					Sequence 4, Appli
					Sequence 41, Appl
					Sequence 119193,
					Sequence 131807,
					Sequence 37454, A
					Sequence 23378, A
					Sequence 19753, A

c	8	17	28.3	1805	18	US-10-424-599-131806	Sequence 131806,
	9	16	26.7	201	21	US-10-741-600-56574	Sequence 56574, A
c	10	16	26.7	382	19	US-10-437-963-75101	Sequence 75101, A
	11	16	26.7	557	9	US-09-878-178-919	Sequence 919, App
	12	16	26.7	557	13	US-10-046-935-919	Sequence 919, App
	13	16	26.7	557	14	US-10-146-503-919	Sequence 919, App
c	14	16	26.7	816	15	US-10-156-761-5190	Sequence 5190, App
c	15	16	26.7	1089	17	US-10-369-493-44330	Sequence 44330, A
c	16	16	26.7	1301	9	US-09-974-300-6140	Sequence 6140, App
c	17	16	26.7	1554	17	US-10-282-122A-17757	Sequence 17757, A
	18	16	26.7	1752	17	US-10-282-122A-41450	Sequence 41450, A
	19	16	26.7	4167	17	US-10-282-122A-33967	Sequence 33967, A
	20	16	26.7	15251	19	US-10-451-467A-669	Sequence 669, App
	21	16	26.7	65300	21	US-10-741-600-17776	Sequence 17776, A
	22	16	26.7	175189	21	US-10-741-600-17738	Sequence 17738, A
c	23	16	26.7	9025608	15	US-10-156-761-1	Sequence 1, Appli
	24	15	25.0	20	21	US-10-831-901A-9924	Sequence 9924, App
	25	15	25.0	20	21	US-10-831-901A-9925	Sequence 9925, App
	26	15	25.0	20	21	US-10-831-901A-9926	Sequence 9926, App
	27	15	25.0	20	21	US-10-831-901A-9927	Sequence 9927, App
	28	15	25.0	20	21	US-10-831-901A-9928	Sequence 9928, App
	29	15	25.0	20	21	US-10-831-901A-9929	Sequence 9929, App
	30	15	25.0	100	17	US-10-242-535A-366	Sequence 366, App
	31	15	25.0	100	18	US-10-085-783A-366	Sequence 366, App
c	32	15	25.0	201	21	US-10-741-600-32304	Sequence 32304, A
c	33	15	25.0	201	21	US-10-741-600-32310	Sequence 32310, A
c	34	15	25.0	201	21	US-10-741-600-32312	Sequence 32312, A
c	35	15	25.0	261	17	US-10-282-122A-36430	Sequence 36430, A
c	36	15	25.0	275	17	US-10-305-720-341	Sequence 341, App
c	37	15	25.0	434	20	US-10-424-599-28755	Sequence 28755, A
c	38	15	25.0	434	20	US-10-425-115-60507	Sequence 60507, A
c	39	15	25.0	448	9	US-09-796-692-8159	Sequence 8159, App
c	40	15	25.0	448	14	US-10-040-862-8159	Sequence 8159, App
c	41	15	25.0	448	17	US-10-057-475B-8159	Sequence 8159, App
c	42	15	25.0	448	17	US-10-154-884B-8159	Sequence 8159, App
c	43	15	25.0	448	19	US-10-764-324-8159	Sequence 8159, App
	44	15	25.0	456	17	US-10-369-493-24810	Sequence 24810, A
c	45	15	25.0	477	10	US-09-814-353-16515	Sequence 16515, A

ALIGNMENTS

RESULT 1  
US-10-057-136-4  
; Sequence 4, Application US/10057136  
; Publication No. US20030021770A1  
; GENERAL INFORMATION:  
; APPLICANT: SCHLOM, JEFFREY  
; APPLICANT: KANTOR, JUDITH  
; APPLICANT: KUFU, DONALD  
; APPLICANT: PANICALI, DENNIS  
; APPLICANT: GRITZ, LINDA  
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1  
; TITLE OF INVENTION: TUMOR-ASSOCIATED ANTIGEN  
; FILE REFERENCE: 700953/47113C  
; CURRENT APPLICATION NUMBER: US/10/057,136  
; CURRENT FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: 09/366,670  
; PRIOR FILING DATE: 1999-08-03  
; PRIOR APPLICATION NUMBER: PCT/US98/03693  
; PRIOR FILING DATE: 1998-02-24  
; PRIOR APPLICATION NUMBER: 60/038,253  
; PRIOR FILING DATE: 1997-02-24  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-057-136-4

Query Match 100.0%; Score 60; DB 14; Length 60;

```
Best Local Similarity 100.0%; Pred. No. 4e-22;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCAGTACTGCACACCGGCACATGGCGTAACATCAGCACCTGATACAAGACCTGCACCT 60
Db 1 GGCAGTACTGCACACCGGCACATGGCGTAACATCAGCACCTGATACAAGACCTGCACCT 60

RESULT 2
US-10-406-317-41
; Sequence 41, Application US/10406317
; Publication No. US20040019195A1
; GENERAL INFORMATION:
; APPLICANT: Schlom, Jeffrey;
; APPLICANT: Hodge, James;
; APPLICANT: Panicali, Dennis
; TITLE OF INVENTION: A recombinant vector expressing multiple constitutatory
; TITLE OF INVENTION: molecules and uses thereof
; FILE REFERENCE: 38163-0189
; CURRENT APPLICATION NUMBER: US/10/406,317
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US/09/856,988
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US99/26866
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/111,582
; PRIOR FILING DATE: 1998-12-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 2297
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VECTOR
; OTHER INFORMATION: SEQUENCE
US-10-406-317-41

Query Match 100.0%; Score 60; DB 17; Length 2297;
Best Local Similarity 100.0%; Pred. No. 3e-22;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCAGTACTGCACACCGGCACATGGCGTAACATCAGCACCTGATACAAGACCTGCACCT 60
Db 406 GGCAGTACTGCACACCGGCACATGGCGTAACATCAGCACCTGATACAAGACCTGCACCT 465

RESULT 3
US-10-424-599-119193/c
; Sequence 119193, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 119193
; LENGTH: 746
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(746)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_7863C.1
US-10-424-599-119193
```

```
Query Match 28.3%; Score 17; DB 18; Length 746;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 CAGCACCTGATACAAGA 51
Db 74 CAGCACCTGATACAAGA 58

RESULT 4
US-10-424-599-131807/c
; Sequence 131807, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 131807
; LENGTH: 863
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_90029C.1
US-10-424-599-131807

Query Match 28.3%; Score 17; DB 18; Length 863;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 CAGCACCTGATACAAGA 51
Db 766 CAGCACCTGATACAAGA 750

RESULT 5
US-10-282-122A-37454/c
; Sequence 37454, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
```



```
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37454
; LENGTH: 891
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-10-282-122A-37454

Query Match      28.3%; Score 17; DB 17; Length 891;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 CCTGATACAAGACCTGC 56
    |||||
Db 224 CCTGATACAAGACCTGC 208

RESULT 6
US-10-282-122A-23378/c
; Sequence 23378, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23378

Query Match      28.3%; Score 17; DB 17; Length 891;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 CCTGATACAAGACCTGC 56
    |||||
Db 224 CCTGATACAAGACCTGC 208

RESULT 7
US-10-282-122A-19753/c
; Sequence 19753, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19753
; LENGTH: 1768
; TYPE: DNA
; ORGANISM: Enterobacter cloacae
US-10-282-122A-19753

Query Match      28.3%; Score 17; DB 17; Length 1768;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTACTGCACCACCGGCA 21
    |||||
Db 663 GTACTGCACCACCGGCA 647

US-10-282-122A-23378
; LENGTH: 1756
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-10-282-122A-23378

Query Match      28.3%; Score 17; DB 17; Length 1756;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTACTGCACCACCGGCA 21
    |||||
Db 663 GTACTGCACCACCGGCA 647
```

RESULT 8  
US-10-424-599-131806/c  
; Sequence 131806, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 131806  
; LENGTH: 1805  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(1805)  
; OTHER INFORMATION: unsure at all n locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_90028C.1  
US-10-424-599-131806

Query Match 28.3%; Score 17; DB 18; Length 1805;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 CAGCACCTGTATACAAGA 51  
|||||  
Db 760 CAGCACCTGTATACAAGA 744

RESULT 9  
US-10-741-600-56574  
; Sequence 56574, Application US/10741600  
; Publication No. US20050026169A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001499  
; CURRENT APPLICATION NUMBER: US/10/741,600  
; CURRENT FILING DATE: 2003-12-22  
; NUMBER OF SEQ ID NOS: 73997  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 56574  
; LENGTH: 201  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-741-600-56574

Query Match 26.7%; Score 16; DB 21; Length 201;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 CCTGATACAAGACCTG 55  
|||||  
Db 44 CCTGATACAAGACCTG 59

RESULT 10  
US-10-437-963-75101/c  
; Sequence 75101, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 75101  
; LENGTH: 382  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_75220C.1  
US-10-437-963-75101

Query Match 26.7%; Score 16; DB 19; Length 382;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 CCTGATACAAGACCTG 55  
|||||  
Db 120 CCTGATACAAGACCTG 105

RESULT 11  
US-09-878-178-919  
; Sequence 919, Application US/09878178  
; Patent No. US20020177552A1  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yuqiu  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Secrist, Heather  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER  
; FILE REFERENCE: 210121.527  
; CURRENT APPLICATION NUMBER: US/09/878,178  
; CURRENT FILING DATE: 2001-06-08  
; NUMBER OF SEQ ID NOS: 2237  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 919  
; LENGTH: 557  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-878-178-919

Query Match 26.7%; Score 16; DB 9; Length 557;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 TACAAGACCTGCACCT 60  
|||||  
Db 541 TACAAGACCTGCACCT 556

RESULT 12  
US-10-046-935-919  
; Sequence 919, Application US/10046935  
; Publication No. US20020156011A1  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Yuqiu  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Secrist, Heather  
; APPLICANT: Wang, Aijun  
; APPLICANT: Stolk, John A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER  
; FILE REFERENCE: 210121.527C1  
; CURRENT APPLICATION NUMBER: US/10/046,935  
; CURRENT FILING DATE: 2002-01-15  
; NUMBER OF SEQ ID NOS: 2239

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 919
; LENGTH: 557
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-046-935-919

Query Match      26.7%; Score 16; DB 13; Length 557;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 TACAAGACCTGCACCT 60
   |||||
Db 541 TACAAGACCTGCACCT 556

RESULT 13
US-10-146-502-919
; Sequence 919, Application US/10146502
; Publication No. US20030069180A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secrist, Heather
; APPLICANT: Wang, Aijun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.527C2
; CURRENT APPLICATION NUMBER: US/10/146,502
; CURRENT FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2241
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 919
; LENGTH: 557
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-146-502-919

Query Match      26.7%; Score 16; DB 14; Length 557;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 TACAAGACCTGCACCT 60
   |||||
Db 541 TACAAGACCTGCACCT 556

RESULT 14
US-10-156-761-5190/c
; Sequence 5190, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 5190
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
```

```
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(816)
US-10-156-761-5190

Query Match      26.7%; Score 16; DB 15; Length 816;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGCACCAACCGGCACA 23
   |||||
Db 30 CTGCACCAACCGGCACA 15

RESULT 15
US-10-369-493-44330/c
; Sequence 44330, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 44330
; LENGTH: 1089
; TYPE: DNA
; ORGANISM: Rhodospseudomonas palustris
US-10-369-493-44330

Query Match      26.7%; Score 16; DB 17; Length 1089;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTACTGCACCAACCGGC 20
   |||||
Db 669 GTACTGCACCAACCGGC 654

Search completed: June 30, 2005, 04:39:50
Job time : 278.7 secs
```

**THIS PAGE BLANK (usptd)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 29, 2005, 19:26:35 ; Search time 51.2 Seconds  
(without alignments)  
1917.512 Million cell updates/sec

Title: US-10-057-136-4  
Perfect score: 60  
Sequence: 1 ggcagtactgcaccaccggc.....ctgatacaagacctgcacct 60

Scoring table:  Gapop 60.0, Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA:  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	17	28.3	1206	4	US-09-489-039A-1114
2	17	28.3	1770	4	US-09-489-039A-1224
3	16	26.7	474	4	US-09-248-796A-4236
4	16	26.7	543	4	US-09-270-767-4523
5	16	26.7	543	4	US-09-270-767-19805
6	16	26.7	601	4	US-09-949-016-136647
7	16	26.7	696	4	US-09-902-540-4831
8	16	26.7	26659	4	US-09-902-540-1237
9	16	26.7	162914	4	US-09-949-016-15578
10	15	25.0	93	4	US-09-270-767-5702
11	15	25.0	93	4	US-09-270-767-20984
12	15	25.0	275	4	US-09-016-434-341
13	15	25.0	421	4	US-09-621-976-2831
14	15	25.0	441	4	US-09-902-540-4058
15	15	25.0	498	4	US-09-252-991A-7343
16	15	25.0	546	3	US-09-643-597-129
17	15	25.0	546	4	US-09-480-884A-129
18	15	25.0	546	4	US-09-542-615A-129
19	15	25.0	546	4	US-09-606-421B-129
20	15	25.0	546	4	US-09-221-107-129
21	15	25.0	546	4	US-09-466-396A-129
22	15	25.0	546	4	US-09-476-496A-129
23	15	25.0	546	4	US-09-630-940B-129
24	15	25.0	546	4	US-09-285-479-129
25	15	25.0	601	4	US-09-949-016-80046
26	15	25.0	601	4	US-09-949-016-80047
27	15	25.0	601	4	US-09-949-016-131978

28	15	25.0	601	4	US-09-949-016-132047
c 29	15	25.0	601	4	US-09-949-016-149501
c 30	15	25.0	601	4	US-09-949-016-149502
31	15	25.0	681	4	US-09-252-991A-7273
32	15	25.0	792	4	US-09-902-540-8829
33	15	25.0	945	4	US-09-252-991A-7152
34	15	25.0	1043	4	US-09-270-767-1158
35	15	25.0	1043	4	US-09-614-221A-174
c 36	15	25.0	1074	4	US-09-270-767-16440
37	15	25.0	1174	2	US-08-793-410-9
c 38	15	25.0	1279	4	US-09-902-540-6180
c 39	15	25.0	1329	4	US-09-252-991A-13223
c 40	15	25.0	1533	4	US-09-949-016-4452
c 41	15	25.0	1959	4	US-09-902-540-313
c 42	15	25.0	2012	2	US-08-555-568B-16
c 43	15	25.0	2012	3	US-09-519-223-16
c 44	15	25.0	2012	4	US-09-927-180-16
c 45	15	25.0	2109	2	US-08-555-568B-20

ALIGNMENTS

RESULT 1  
US-09-489-039A-1114  
; Sequence 1114, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 1114  
; LENGTH: 1206  
; TYPE: DNA  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-1114

Query Match 28.3%; Score 17; DB 4; Length 1206;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTACTGCACCACCGGCA 21  
|||||  
Db 1132 GTACTGCACCACCGGCA 1148

RESULT 2  
US-09-489-039A-1224/c  
; Sequence 1224, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 1224  
; LENGTH: 1770  
; TYPE: DNA  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-1224

Query Match 28.3%; Score 17; DB 4; Length 1770;

```
Best Local Similarity 100.0%; Pred. No. 11;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTACTGCACCGCGCA 21
    |||||
Db 639 GTACTGCACCGCGCA 623

RESULT 3
US-09-248-796A-4236
; Sequence 4236, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 4236
; LENGTH: 474
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-4236

Query Match 26.7%; Score 16; DB 4; Length 474;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 GTAACATCAGCACCTG 43
    |||||
Db 130 GTAACATCAGCACCTG 145

RESULT 4
US-09-270-767-4523/c
; Sequence 4523, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4523
; LENGTH: 543
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-4523

Query Match 26.7%; Score 16; DB 4; Length 543;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CACCACCGGCACATGG 26
    |||||
Db 238 CACCACCGGCACATGG 223

RESULT 5
US-09-270-767-19805/c
; Sequence 19805, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
```

```
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19805
LENGTH: 543
TYPE: DNA
ORGANISM: Drosophila melanogaster
US-09-270-767-19805

Query Match 26.7%; Score 16; DB 4; Length 543;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CACCACCGGCACATGG 26
    |||||
Db 238 CACCACCGGCACATGG 223

RESULT 6
US-09-949-016-136647/c
; Sequence 136647, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136647
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-136647

Query Match 26.7%; Score 16; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 TCAGCACCTGATACAA 49
    |||||
Db 150 TCAGCACCTGATACAA 135

RESULT 7
US-09-902-540-4831/c
; Sequence 4831, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 4831
; LENGTH: 696
; TYPE: DNA
```

```
; ORGANISM: Myxococcus xanthus
US-09-902-540-4831

Query Match      26.7%; Score 16; DB 4; Length 696;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 GCACCACCGGCACATG 25
Db      514 GCACCACCGGCACATG 499

RESULT 8
US-09-902-540-1237
; Sequence 1237, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1237
; LENGTH: 26659
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1237

Query Match      26.7%; Score 16; DB 4; Length 26659;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 GCACCACCGGCACATG 25
Db      6906 GCACCACCGGCACATG 6921

RESULT 9
US-09-949-016-15578
; Sequence 15578, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15578
; LENGTH: 162914
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(162914)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15578

Query Match      26.7%; Score 16; DB 4; Length 162914;
```

```
; ORGANISM: Drosophila melanogaster
US-09-270-767-5702
; Sequence 5702, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5702
; LENGTH: 93
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-5702

Query Match      25.0%; Score 15; DB 4; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CTGCACCACCGGCAC 22
Db      34 CTGCACCACCGGCAC 48

RESULT 11
US-09-270-767-20984
; Sequence 20984, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20984
; LENGTH: 93
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-20984

Query Match      25.0%; Score 15; DB 4; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CTGCACCACCGGCAC 22
Db      34 CTGCACCACCGGCAC 48

RESULT 12
US-09-016-434-341/c
; Sequence 341, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
```

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/016,434  
; FILING DATE: HERewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0002 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 341:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 275 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: BRSTNOT04  
; CLONE: 1963772  
; US-09-016-434-341

Query Match 25.0%; Score 15; DB 4; Length 275;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 AACATCAGCACCTGA 44  
Db 91 AACATCAGCACCTGA 77  
RESULT 13  
US-09-621-976-2831/c  
; Sequence 2831, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 2831  
; LENGTH: 421  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 79..228  
; US-09-621-976-2831

Query Match 25.0%; Score 15; DB 4; Length 421;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 TAACATCAGCACCTG 43  
Db 334 TAACATCAGCACCTG 320  
RESULT 14  
US-09-902-540-4058/c  
; Sequence 4058, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 4058  
; LENGTH: 441  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
; US-09-902-540-4058

Query Match 25.0%; Score 15; DB 4; Length 441;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GCACCACCGGCACAT 24  
Db 151 GCACCACCGGCACAT 137

RESULT 15  
US-09-252-991A-7343/c  
; Sequence 7343, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 7343  
; LENGTH: 498  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
; US-09-252-991A-7343

Query Match 25.0%; Score 15; DB 4; Length 498;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTGCACCACCGGCAC 22  
Db 420 CTGCACCACCGGCAC 406

Search completed: June 30, 2005, 04:02:33  
Job time : 129.2 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 29, 2005, 23:23:45 ; Search time 230.7 Seconds  
(without alignments)  
1625.622 Million cell updates/sec

Title: US-10-057-136-6  
Perfect score: 60  
Sequence: 1 gggtaacagctcctccgc.....cagatactgcccagctcca 60

Scoring table:  Gapop 60.0 , Gapext 60.0

Searched: 6067389 seqs, 3125258755 residues

Word size : 0

Total number of hits satisfying chosen parameters: 12134778

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:  
9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:  
13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:  
14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:  
15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:  
16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:  
17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:  
18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:  
19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq:  
20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq:  
21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq:  
22: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:  
23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq:  
24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:  
25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:  
26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	100.0	60	14	US-10-057-136-6
2	60	100.0	2297	17	US-10-406-317-41
3	20	33.3	201	21	US-10-741-600-3612
4	20	33.3	201	21	US-10-741-600-3628
5	20	33.3	201	21	US-10-741-600-3676
6	20	33.3	405	9	US-09-867-701-1712
7	20	33.3	453	21	US-10-926-683-517
					Sequence 6, Appli
					Sequence 41, Appl
					Sequence 3612, Ap
					Sequence 3628, Ap
					Sequence 3676, Ap
					Sequence 1712, Ap
					Sequence 517, App

c	8	20	33.3	1405	21	US-10-741-600-65	Sequence 65, Appl
c	9	20	33.3	2655	21	US-10-741-600-62	Sequence 62, Appl
c	10	20	33.3	2659	21	US-10-741-600-61	Sequence 61, Appl
c	11	20	33.3	16747	21	US-10-741-600-17923	Sequence 17923, A
c	12	20	33.3	27875	21	US-10-741-600-17578	Sequence 17578, A
c	13	18	30.0	1228	19	US-10-437-963-97051	Sequence 97051, A
c	14	18	30.0	2493	19	US-10-437-963-97047	Sequence 97047, A
	15	18	30.0	3899	9	US-09-735-367B-5	Sequence 5, Appli
	16	18	30.0	6504	9	US-09-969-347-171	Sequence 171, Appl
	17	18	30.0	6504	9	US-09-735-367B-9	Sequence 9, Appli
	18	18	30.0	6504	21	US-10-843-641A-8300	Sequence 8300, Ap
	19	18	30.0	6878	9	US-09-735-367B-1	Sequence 1, Appli
	20	17	28.3	230	20	US-10-357-930-15001	Sequence 15001, A
c	21	17	28.3	252	16	US-10-029-386-26242	Sequence 26242, A
c	22	17	28.3	312	17	US-10-282-122A-35901	Sequence 35901, A
c	23	17	28.3	502	20	US-10-357-930-39111	Sequence 39111, A
	24	17	28.3	502	20	US-10-357-930-44897	Sequence 44897, A
c	25	17	28.3	556	16	US-10-029-386-12542	Sequence 12542, A
c	26	17	28.3	1470	17	US-10-282-122A-33548	Sequence 33548, A
c	27	17	28.3	1809	18	US-10-267-502-97	Sequence 97, Appl
c	28	17	28.3	3048	18	US-10-641-643-957	Sequence 957, App
c	29	17	28.3	256157	13	US-10-087-192-1204	Sequence 1204, Ap
	30	17	28.3	256157	19	US-10-322-281-776	Sequence 776, App
c	31	16	26.7	542	13	US-10-027-632-283188	Sequence 283188,
c	32	16	26.7	542	17	US-10-027-632-283188	Sequence 283188,
c	33	16	26.7	550	17	US-10-388-934-766	Sequence 766, App
c	34	16	26.7	663	18	US-10-404-460-13	Sequence 13, Appl
c	35	16	26.7	1233	13	US-10-027-632-123149	Sequence 123149,
c	36	16	26.7	1233	17	US-10-027-632-123149	Sequence 123149,
c	37	16	26.7	1508	19	US-10-437-963-102285	Sequence 102285,
c	38	16	26.7	1644	16	US-10-060-521-3	Sequence 3, Appli
c	39	16	26.7	1889	10	US-09-932-300-108	Sequence 108, App
c	40	16	26.7	4403	17	US-10-398-221-3755	Sequence 3755, Ap
c	41	16	26.7	4722	19	US-10-437-963-74767	Sequence 74767, A
c	42	16	26.7	8961	17	US-10-062-674-1474	Sequence 1474, Ap
c	43	16	26.7	60327	18	US-10-052-482-187	Sequence 187, App
c	44	16	26.7	77777	19	US-10-318-389-4	Sequence 4, Appli
c	45	16	26.7	79860	13	US-10-087-192-412	Sequence 412, App

ALIGNMENTS

RESULT 1  
US-10-057-136-6  
; Sequence 6, Application US/10057136  
; Publication No. US20030021770A1  
; GENERAL INFORMATION:  
; APPLICANT: SCHLOM, JEFFREY  
; APPLICANT: KANTOR, JUDITH  
; APPLICANT: KUFU, DONALD  
; APPLICANT: PANICALI, DENNIS  
; APPLICANT: GRITZ, LINDA  
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1  
; TITLE OF INVENTION: TUMOR-ASSOCIATED ANTIGEN  
; FILE REFERENCE: 700953/47113C  
; CURRENT APPLICATION NUMBER: US/10/057,136  
; CURRENT FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: 09/366,670  
; PRIOR FILING DATE: 1999-08-03  
; PRIOR APPLICATION NUMBER: PCT/US98/03693  
; PRIOR FILING DATE: 1998-02-24  
; PRIOR APPLICATION NUMBER: 60/038,253  
; PRIOR FILING DATE: 1997-02-24  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-057-136-6  
Query Match 100.0%; Score 60; DB 14; Length 60;

Best Local Similarity 100.0%; Pred. No. 8.3e-24;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTCAACAGCTCTCCCGCTCATGGGGTTACTTCTGCTCCAGATACTCGCCAGCTCCA 60  
Db 1 GGGTCAACAGCTCTCCCGCTCATGGGGTTACTTCTGCTCCAGATACTCGCCAGCTCCA 60

RESULT 2  
US-10-406-317-41  
; Sequence 41, Application US/10406317  
; Publication No. US20040019195A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlom, Jeffrey;  
; APPLICANT: Panicali, Dennis  
; TITLE OF INVENTION: A recombinant vector expressing multiple constitutulatory  
; TITLE OF INVENTION: molecules and uses thereof  
; FILE REFERENCE: 38163-0189  
; CURRENT APPLICATION NUMBER: US/10/406,317  
; CURRENT FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: US/09/856,988  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: PCT/US99/26866  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/111,582  
; PRIOR FILING DATE: 1998-12-09  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 41  
; LENGTH: 2297  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: VECTOR  
US-10-406-317-41

Query Match 100.0%; Score 60; DB 17; Length 2297;  
Best Local Similarity 100.0%; Pred. No. 6.6e-24;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTCAACAGCTCTCCCGCTCATGGGGTTACTTCTGCTCCAGATACTCGCCAGCTCCA 60  
Db 526 GGGTCAACAGCTCTCCCGCTCATGGGGTTACTTCTGCTCCAGATACTCGCCAGCTCCA 585

RESULT 3  
US-10-741-600-3612/c  
; Sequence 3612, Application US/10741600  
; Publication No. US20050026169A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001499  
; CURRENT APPLICATION NUMBER: US/10/741,600  
; CURRENT FILING DATE: 2003-12-22  
; NUMBER OF SEQ ID NOS: 73997  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3612  
; LENGTH: 201  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-741-600-3612

Query Match 33.3%; Score 20; DB 21; Length 201;  
Best Local Similarity 100.0%; Pred. No. 0.27;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 CTCAGATACTCGCCAGCT 57  
Db 45 CTCAGATACTCGCCAGCT 26

RESULT 4  
US-10-741-600-3628/c  
; Sequence 3628, Application US/10741600  
; Publication No. US20050026169A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001499  
; CURRENT APPLICATION NUMBER: US/10/741,600  
; CURRENT FILING DATE: 2003-12-22  
; NUMBER OF SEQ ID NOS: 73997  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3628  
; LENGTH: 201  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-741-600-3628

Query Match 33.3%; Score 20; DB 21; Length 201;  
Best Local Similarity 100.0%; Pred. No. 0.27;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 CTCAGATACTCGCCAGCT 57  
Db 45 CTCAGATACTCGCCAGCT 26

RESULT 5  
US-10-741-600-3676/c  
; Sequence 3676, Application US/10741600  
; Publication No. US20050026169A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001499  
; CURRENT APPLICATION NUMBER: US/10/741,600  
; CURRENT FILING DATE: 2003-12-22  
; NUMBER OF SEQ ID NOS: 73997  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3676  
; LENGTH: 201  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-741-600-3676

Query Match 33.3%; Score 20; DB 21; Length 201;  
Best Local Similarity 100.0%; Pred. No. 0.27;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 CTCAGATACTCGCCAGCT 57  
Db 45 CTCAGATACTCGCCAGCT 26

RESULT 6  
US-09-867-701-1712/c  
; Sequence 1712, Application US/09867701  
; Patent No. US20020132237A1  
; GENERAL INFORMATION:  
; APPLICANT: Aglate, Paul A.  
; APPLICANT: Harlocker, Susan L.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER  
; FILE REFERENCE: 210121.497  
; CURRENT APPLICATION NUMBER: US/09/867,701  
; CURRENT FILING DATE: 2001-05-29  
; NUMBER OF SEQ ID NOS: 10912  
; SOFTWARE: FastSeq for Windows Version 4.0

```

; SEQ ID NO 1712
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(405)
; OTHER INFORMATION: n = A,T,C or G
US-09-867-701-1712

Query Match      33.3%; Score 20; DB 9; Length 405;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CTCAGATACGCCCCAGCT 57
   |||||
Db 33 CTCAGATACGCCCCAGCT 14

RESULT 7
US-10-926-683-517/c
; Sequence 517, Application US/10926683
; Publication No. US20050106595A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: GENSET.025CP1
; CURRENT APPLICATION NUMBER: US/10/926,683
; CURRENT FILING DATE: 2004-08-25
; PRIOR APPLICATION NUMBER: US/09/471,276
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 09/057,719
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 09/069,047
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: PCT/IB99/00712
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 517
; LENGTH: 453
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 113..451
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 113..307
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 4.4000009536743
; OTHER INFORMATION: seq FIEAALLINGSAC/VY
US-10-926-683-517

Query Match      33.3%; Score 20; DB 21; Length 453;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CTCAGATACGCCCCAGCT 57
   |||||
Db 217 CTCAGATACGCCCCAGCT 198

RESULT 8
US-10-741-600-65/c
; Sequence 65, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

```

```

; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 1405
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-65

Query Match      33.3%; Score 20; DB 21; Length 1405;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CTCAGATACGCCCCAGCT 57
   |||||
Db 200 CTCAGATACGCCCCAGCT 181

RESULT 9
US-10-741-600-62/c
; Sequence 62, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 2655
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-62

Query Match      33.3%; Score 20; DB 21; Length 2655;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CTCAGATACGCCCCAGCT 57
   |||||
Db 296 CTCAGATACGCCCCAGCT 277

RESULT 10
US-10-741-600-61/c
; Sequence 61, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 2659
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-61

Query Match      33.3%; Score 20; DB 21; Length 2659;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CTCAGATACGCCCCAGCT 57
   |||||

```

Db 296 CTCCAGATACTGCCCCAGCT 277

RESULT 11

US-10-741-600-17923

; Sequence 17923, Application US/10741600

; Publication No. US20050026169A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001499

; CURRENT APPLICATION NUMBER: US/10/741,600

; CURRENT FILING DATE: 2003-12-22

; NUMBER OF SEQ ID NOS: 73997

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 17923

; LENGTH: 16747

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-741-600-17923

Query Match 33.3%; Score 20; DB 21; Length 16747;

Best Local Similarity 100.0%; Pred. No. 0.2;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 CTCCAGATACTGCCCCAGCT 57

Db 5253 CTCCAGATACTGCCCCAGCT 5272

RESULT 12

US-10-741-600-17578/c

; Sequence 17578, Application US/10741600

; Publication No. US20050026169A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001499

; CURRENT APPLICATION NUMBER: US/10/741,600

; CURRENT FILING DATE: 2003-12-22

; NUMBER OF SEQ ID NOS: 73997

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 17578

; LENGTH: 27875

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(27875)

; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-10)

US-10-741-600-17578

Query Match 33.3%; Score 20; DB 21; Length 27875;

Best Local Similarity 100.0%; Pred. No. 0.2;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 CTCCAGATACTGCCCCAGCT 57

Db 6295 CTCCAGATACTGCCCCAGCT 6276

RESULT 13

US-10-437-963-97051/c

; Sequence 97051, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: RICE NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 97051

; LENGTH: 1228

; TYPE: DNA

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_95091C.1

US-10-437-963-97051

Query Match 30.0%; Score 18; DB 19; Length 1228;

Best Local Similarity 100.0%; Pred. No. 3.2;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 ACTTCTGCTCCAGATACT 48

Db 720 ACTTCTGCTCCAGATACT 703

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 97051

; LENGTH: 1228

; TYPE: DNA

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_95091C.1

US-10-437-963-97051

Query Match 30.0%; Score 18; DB 19; Length 1228;

Best Local Similarity 100.0%; Pred. No. 3.2;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 ACTTCTGCTCCAGATACT 48

Db 720 ACTTCTGCTCCAGATACT 703

RESULT 14

US-10-437-963-97047/c

; Sequence 97047, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 97047

; LENGTH: 2493

; TYPE: DNA

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_95088C.1

US-10-437-963-97047

Query Match 30.0%; Score 18; DB 19; Length 2493;

Best Local Similarity 100.0%; Pred. No. 3.1;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 ACTTCTGCTCCAGATACT 48

Db 2416 ACTTCTGCTCCAGATACT 2399

RESULT 15

US-09-735-367B-5

; Sequence 5, Application US/09735367B

; Patent No. US20020151477A1

; GENERAL INFORMATION:

; APPLICANT: Gustafsson, Jan-Ake

; APPLICANT: Caira, Francoise

; APPLICANT: Antonsson, Per

; TITLE OF INVENTION: NUCLEAR RECEPTOR COACTIVATOR

; FILE REFERENCE: 102093-100

; CURRENT APPLICATION NUMBER: US/09/735,367B

```
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US 60/174,544
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 3899
; TYPE: DNA
; ORGANISM: mammal
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (203)...(3415)
US-09-735-367B-5
```

```
Query Match      30.0%; Score 18; DB 9; Length 3899;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      40 CCAGATACTCGCCGAGCT 57
        |||||
Db      2999 CCAGATACTCGCCGAGCT 3016
```

```
Search completed: June 30, 2005, 04:44:46
Job time : 358.7 secs
```

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 29, 2005, 19:26:35 ; Search time 51.2 Seconds  
(without alignments)  
1917.512 Million cell updates/sec

Title: US-10-057-136-6  
Perfect score: 60  
Sequence: 1 gggtaacagctcctccgc.....cagatactgcccagctcca 60

Scoring table:   
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA:\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
C 1	20	33.3	453	4	US-09-471-276-517
C 2	20	33.3	511	4	US-09-621-976-1594
C 3	17	28.3	3048	4	US-09-023-655-957
C 4	17	28.3	240157	4	US-09-949-016-16264
C 5	16	26.7	1512	4	US-09-270-767-15148
C 6	16	26.7	27617	4	US-09-949-016-17040
C 7	16	26.7	246444	4	US-09-949-016-13113
C 8	15	25.0	30	1	US-08-410-739-1
C 9	15	25.0	30	1	US-08-697-815-1
C 10	15	25.0	30	2	US-09-061-286-1
C 11	15	25.0	327	4	US-09-313-294A-7059
C 12	15	25.0	375	4	US-09-513-999C-13614
C 13	15	25.0	415	4	US-09-270-767-30904
C 14	15	25.0	417	4	US-09-513-999C-10290
C 15	15	25.0	488	4	US-09-513-999C-10293
C 16	15	25.0	601	4	US-09-949-016-39033
C 17	15	25.0	601	4	US-09-949-016-142149
C 18	15	25.0	601	4	US-09-949-016-158466
C 19	15	25.0	601	4	US-09-949-016-158467
C 20	15	25.0	601	4	US-09-949-016-158468
C 21	15	25.0	601	4	US-09-949-016-178512
C 22	15	25.0	822	4	US-09-023-655-1078
C 23	15	25.0	874	4	US-09-513-999C-14943
C 24	15	25.0	888	4	US-09-949-016-4424
C 25	15	25.0	947	4	US-09-919-039-332
C 26	15	25.0	1186	4	US-09-513-999C-14929
C 27	15	25.0	1325	4	US-09-566-921-131

C 28	15	25.0	1629	3	US-08-939-309-5	Sequence 5, Appli
C 29	15	25.0	1629	4	US-09-849-180-5	Sequence 5, Appli
C 30	15	25.0	1629	4	US-09-356-643B-3	Sequence 3, Appli
C 31	15	25.0	1629	4	US-10-053-510-3	Sequence 3, Appli
C 32	15	25.0	1827	4	US-09-602-787A-29	Sequence 29, Appli
C 33	15	25.0	2212	4	US-09-270-767-14682	Sequence 14682, A
C 34	15	25.0	2697	4	US-09-949-016-5116	Sequence 5116, Ap
C 35	15	25.0	3401	4	US-09-907-794A-249	Sequence 249, App
C 36	15	25.0	3401	4	US-09-905-125A-249	Sequence 249, App
C 37	15	25.0	3401	4	US-09-902-775A-249	Sequence 249, App
C 38	15	25.0	3401	4	US-09-906-700-249	Sequence 249, App
C 39	15	25.0	3401	4	US-09-903-603A-249	Sequence 249, App
C 40	15	25.0	3401	4	US-09-904-920A-249	Sequence 249, App
C 41	15	25.0	3401	4	US-09-909-064-249	Sequence 249, App
C 42	15	25.0	3401	4	US-09-905-381A-249	Sequence 249, App
C 43	15	25.0	3401	4	US-09-906-618-249	Sequence 249, App
C 44	15	25.0	3747	2	US-09-080-897-1	Sequence 1, Appli
C 45	15	25.0	3747	3	US-09-323-735-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1  
US-09-471-276-517/c  
; Sequence 517, Application US/09471276  
; Patent No. 6822072  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6822072  
; FILE REFERENCE: GENSET.025CP1  
; CURRENT APPLICATION NUMBER: US/09/471,276  
; CURRENT FILING DATE: 1999-12-21  
; EARLIER APPLICATION NUMBER: 09/057,719  
; EARLIER FILING DATE: 1998-04-09  
; EARLIER APPLICATION NUMBER: 09/069,047  
; EARLIER FILING DATE: 1998-04-28  
; EARLIER APPLICATION NUMBER: PCT/IB99/00712  
; EARLIER FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 1622  
; SOFTWARE: Patent.pm  
; SEQ ID NO 517  
; LENGTH: 453  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 113..451  
; NAME/KEY: sig peptide  
; LOCATION: 113..307  
; OTHER INFORMATION: Von Heijne matrix  
; OTHER INFORMATION: score 4.4000009536743  
; OTHER INFORMATION: seq FIEAALLIHGSAC/VY  
US-09-471-276-517

Query Match 33.3%; Score 20; DB 4; Length 453;  
Best Local Similarity 100.0%; Pred. No. 0.48;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 38 CTCCAGATACGCCCCAGCT 57  
|||||  
Db 217 CTCCAGATACGCCCCAGCT 198

RESULT 2  
US-09-621-976-1594/c  
; Sequence 1594, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.

```

; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 1594
; LENGTH: 511
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 99..443
; NAME/KEY: sig_peptide
; LOCATION: 99..293
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 5.90000009536743
; OTHER INFORMATION: seq FIEAALLIQSAA/ST
US-09-621-976-1594

Query Match      33.3%; Score 20; DB 4; Length 511;
Best Local Similarity 100.0%; Pred. No. 0.48;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 CTCGAGATACGCGCCAGCT 57
Db 203 CTCGAGATACGCGCCAGCT 184

RESULT 3
US-09-023-655-957/c
; Sequence 957, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 957:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3048 base pairs
; TYPE: nucleic acid

```

```

; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1478067
US-09-023-655-957

Query Match      28.3%; Score 17; DB 4; Length 3048;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AACAGCTCTCCCGCTC 22
Db 540 AACAGCTCTCCCGCTC 524

RESULT 4
US-09-949-016-16264
; Sequence 16264, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16264
; LENGTH: 240157
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(240157)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16264

Query Match      28.3%; Score 17; DB 4; Length 240157;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 ACTTCTGCTCCAGATAC 47
Db 104643 ACTTCTGCTCCAGATAC 104659

RESULT 5
US-09-270-767-15148/c
; Sequence 15148, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15148
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-15148

Query Match      26.7%; Score 16; DB 4; Length 1512;

```



```
Best Local Similarity 100.0%; Pred. No. 55;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AACAGCTCCTCCGGCT 21
Db 611 AACAGCTCCTCCGGCT 596

RESULT 6
US-09-949-016-17040/c
; Sequence 17040, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17040
; LENGTH: 27617
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17040

Query Match 26.7%; Score 16; DB 4; Length 27617;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 CTTCTGCTCCGATAC 47
Db 2810 CTTCTGCTCCGATAC 2795

RESULT 7
US-09-949-016-13113/c
; Sequence 13113, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13113
; LENGTH: 246444
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(246444)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13113

Query Match 26.7%; Score 16; DB 4; Length 246444;
Best Local Similarity 100.0%; Pred. No. 57;
```

```
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 TACTTCTGCTCCAGAT 45
Db 193625 TACTTCTGCTCCAGAT 193610

RESULT 8
US-08-410-739-1/c
; Sequence 1, Application US/08410739
; Patent No. 5759836
; GENERAL INFORMATION:
; APPLICANT: AMIN, Ashok R.
; APPLICANT: ABRAMSON, Steven B.
; TITLE OF INVENTION: A NOVEL NITRIC OXIDE SYNTHASE,
; TITLE OF INVENTION: ANTIBODIES THERETO AND METHOD OF SCREENING COMPOUNDS FOR
; TITLE OF INVENTION: INHIBITION OF SAME
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,739
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: YUN, Allen C.
; REGISTRATION NUMBER: 37,971
; REFERENCE/DOCKET NUMBER: AMIN=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-410-739-1

Query Match 25.0%; Score 15; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 ACTTCTGCTCCAGAT 45
Db 29 ACTTCTGCTCCAGAT 15

RESULT 9
US-08-697-815-1/c
; Sequence 1, Application US/08697815
; Patent No. 5789395
; GENERAL INFORMATION:
; APPLICANT: Amin, Ashok R.
; APPLICANT: Abramson, Steven B.
; APPLICANT: Golub, Lorne M.
; APPLICANT: Ramamurthy, Nungavaram S.
; APPLICANT: McNamara, Thomas F.
; APPLICANT: Greenwald, Robert
; APPLICANT: Trachtman, Howard
; TITLE OF INVENTION: Method of Using Tetracycline Compounds
```

; TITLE OF INVENTION: for Inhibition of Nitric Oxide Production  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOFFMANN & BARON  
; STREET: 350 Jericho Turnpike  
; CITY: Jericho  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 11753  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/697,815  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: O'Dea, Sean W  
; REGISTRATION NUMBER: 37,690  
; REFERENCE/DOCKET NUMBER: 178-218  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 822-3550  
; TELEFAX: (516) 822-3582  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 30 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; US-08-697-815-1

Query Match 25.0%; Score 15; DB 1; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 ACTTCTGCTCCAGAT 45  
|||||  
Db 29 ACTTCTGCTCCAGAT 15

RESULT 10  
US-09-061-286-1/c  
; Sequence 1, Application US/09061286  
; Patent No. 5919775  
; GENERAL INFORMATION:  
; APPLICANT: Amin, Ashok R  
; APPLICANT: Abramson, Steven B  
; APPLICANT: Golub, Lorne M  
; APPLICANT: Ramamurthy, Nungavaram S  
; APPLICANT: McNamara, Thomas F  
; APPLICANT: Greenwald, Robert  
; APPLICANT: Trachtman, Howard  
; TITLE OF INVENTION: Method of Using Tetracycline  
; TITLE OF INVENTION: Compounds For Inhibition of Nitric Oxide Production  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HOFFMANN & BARON, LLP  
; STREET: 350 Jericho Turnpike  
; CITY: Jericho  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 11753  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/061,286  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/697,815  
; FILING DATE: 30-AUGUST-1996  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: O'Dea, Sean W.  
; REGISTRATION NUMBER: 37690  
; REFERENCE/DOCKET NUMBER: 178-218 DIV  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 822-3550  
; TELEFAX: (516) 822-3582  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 30 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; US-09-061-286-1

Query Match 25.0%; Score 15; DB 2; Length 30;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 ACTTCTGCTCCAGAT 45  
|||||  
Db 29 ACTTCTGCTCCAGAT 15

RESULT 11  
US-09-313-294A-7059/c  
; Sequence 7059, Application US/09313294A  
; Patent No. 6476212  
; GENERAL INFORMATION:  
; APPLICANT: Lalgudi, Raghunath V.  
; APPLICANT: Ito, Laura Y.  
; APPLICANT: Sherman, Bradley K.  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR  
; FILE REFERENCE: PL-0017 US  
; CURRENT APPLICATION NUMBER: US/09/313,294A  
; CURRENT FILING DATE: 1999-05-14  
; NUMBER OF SEQ ID NOS: 7600  
; SOFTWARE: PERL Program  
; SEQ ID NO 7059  
; LENGTH: 327  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. 6476212 700381058H1  
; NAME/KEY: unsure  
; LOCATION: 28,162, 275  
; OTHER INFORMATION: a, t, c, g, or other  
; US-09-313-294A-7059

Query Match 25.0%; Score 15; DB 4; Length 327;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 AGATACTCGCCGAGC 56  
|||||  
Db 271 AGATACTCGCCGAGC 257

RESULT 12  
US-09-513-999C-13614/c  
; Sequence 13614, Application US/09513999C  
; Patent No. 6783961

```

; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 13614
; LENGTH: 375
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-13614

Query Match      25.0%; Score 15; DB 4; Length 375;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 ACAGCTCCTCCGCT 21
Db      132 ACAGCTCCTCCGCT 118

RESULT 13
US-09-270-767-30904/c
; Sequence 30904, Application US/09270767.
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 30904
; LENGTH: 415
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-30904

Query Match      25.0%; Score 15; DB 4; Length 415;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CAGCTCCTCCGCTC 22
Db      280 CAGCTCCTCCGCTC 266

RESULT 14
US-09-513-999C-10290/c
; Sequence 10290, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 10290

```

```

; LENGTH: 417
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 6
; OTHER INFORMATION: n=a, g, c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 200
; OTHER INFORMATION: m=a or c
US-09-513-999C-10290

Query Match      25.0%; Score 15; DB 4; Length 417;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      42 AGATACTCGCCGAGC 56
Db      271 AGATACTCGCCGAGC 257

RESULT 15
US-09-513-999C-10293/c
; Sequence 10293, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 10293
; LENGTH: 488
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 6
; OTHER INFORMATION: n=a, g, c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 271
; OTHER INFORMATION: m=a or c
US-09-513-999C-10293

Query Match      25.0%; Score 15; DB 4; Length 488;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      42 AGATACTCGCCGAGC 56
Db      342 AGATACTCGCCGAGC 328

Search completed: June 30, 2005, 04:04:22
Job time : 90.2 secs

```

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 29, 2005, 23:23:45 ; Search time 230.7 Seconds  
(without alignments)  
1625.622 Million cell updates/sec

Title: US-10-057-136-7  
Perfect score: 60  
Sequence: 1 ggttcgacggccccctgc.....cggataccagcggccct 60

Scoring table:  Gapop 60.0, Gapext 60.0

Searched: 6067389 seqs, 3125258755 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 12134778

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:  
9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:  
13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:  
14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:  
15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:  
16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:  
17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:  
18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:  
19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq:  
20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq:  
21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq:  
22: /cgn2\_6/ptodata/1/pubpna/US10J\_PUBCOMB.seq:  
23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq:  
24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:  
25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:  
26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	100.0	60	14	US-10-057-136-7
2	60	100.0	2297	17	US-10-406-317-41
3	17	28.3	867	17	US-10-369-493-33682
4	17	28.3	1171	20	US-10-425-115-66540
5	16	26.7	406	10	US-09-918-995-36727
6	16	26.7	465	10	US-09-918-995-32117
7	16	26.7	769	20	US-10-425-115-92232
					Sequence 7, Appli
					Sequence 41, Appl
					Sequence 33682, A
					Sequence 66540, A
					Sequence 36727, A
					Sequence 32117, A
					Sequence 92232, A

c	8	16	26.7	1153	15	US-10-106-698-1517	Sequence 1517, Ap
c	9	16	26.7	1194	17	US-10-369-493-38104	Sequence 38104, A
c	10	16	26.7	2064	17	US-10-369-493-35087	Sequence 35087, A
c	11	16	26.7	2064	17	US-10-369-493-38514	Sequence 38514, A
c	12	16	26.7	2088	17	US-10-369-493-38696	Sequence 38696, A
c	13	16	26.7	3285	9	US-09-712-363-143	Sequence 143, App
c	14	16	26.7	31718	10	US-09-764-872-812	Sequence 812, App
c	15	16	26.7	31718	10	US-09-764-872-813	Sequence 813, App
c	16	16	26.7	31718	10	US-09-764-891-9103	Sequence 9103, Ap
c	17	16	26.7	31718	10	US-09-764-891-9104	Sequence 9104, Ap
c	18	16	26.7	31718	11	US-09-973-278-787	Sequence 787, App
c	19	16	26.7	31718	11	US-09-973-278-788	Sequence 788, App
c	20	15	25.0	170	18	US-10-452-858C-16	Sequence 16, Appl
c	21	15	25.0	306	20	US-10-425-115-34287	Sequence 34287, A
c	22	15	25.0	353	20	US-10-425-115-36307	Sequence 36307, A
c	23	15	25.0	491	18	US-10-425-114-23480	Sequence 23480, A
c	24	15	25.0	535	20	US-10-357-930-2843	Sequence 2843, Ap
c	25	15	25.0	546	20	US-10-425-115-174502	Sequence 174502,
c	26	15	25.0	566	19	US-10-437-963-74836	Sequence 74836, A
c	27	15	25.0	570	20	US-10-357-930-33184	Sequence 33184, A
c	28	15	25.0	570	20	US-10-357-930-42109	Sequence 42109, A
c	29	15	25.0	675	15	US-10-156-761-5648	Sequence 5648, Ap
c	30	15	25.0	718	20	US-10-357-930-21830	Sequence 21830, A
c	31	15	25.0	718	20	US-10-357-930-27677	Sequence 27677, A
c	32	15	25.0	742	13	US-10-027-632-29386	Sequence 29386, A
c	33	15	25.0	742	13	US-10-027-632-29387	Sequence 29387, A
c	34	15	25.0	742	17	US-10-027-632-29386	Sequence 29386, A
c	35	15	25.0	742	17	US-10-027-632-29387	Sequence 29387, A
c	36	15	25.0	830	20	US-10-425-115-21091	Sequence 21091, A
c	37	15	25.0	852	13	US-10-027-632-134229	Sequence 134229,
c	38	15	25.0	852	13	US-10-027-632-134230	Sequence 134230,
c	39	15	25.0	852	17	US-10-027-632-134229	Sequence 134229,
c	40	15	25.0	852	17	US-10-027-632-134230	Sequence 134230,
c	41	15	25.0	853	20	US-10-357-930-12012	Sequence 12012, A
c	42	15	25.0	900	20	US-10-425-115-179856	Sequence 179856,
c	43	15	25.0	1035	15	US-10-156-761-1799	Sequence 1799, Ap
c	44	15	25.0	1252	19	US-10-767-701-14257	Sequence 14257, A
c	45	15	25.0	2000	18	US-10-433-238-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1  
US-10-057-136-7  
; Sequence 7, Application US/10057136  
; Publication No. US20030021770A1  
; GENERAL INFORMATION:  
; APPLICANT: SCHLOM, JEFFREY  
; APPLICANT: KANTOR, JUDITH  
; APPLICANT: KUFU, DONALD  
; APPLICANT: PANICALI, DENNIS  
; APPLICANT: GRITZ, LINDA  
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1  
; TITLE OF INVENTION: TUMOR-ASSOCIATED ANTIGEN  
; FILE REFERENCE: 700953/47113C  
; CURRENT APPLICATION NUMBER: US/10/057,136  
; CURRENT FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: 09/366,670  
; PRIOR FILING DATE: 1999-08-03  
; PRIOR APPLICATION NUMBER: PCT/US98/03693  
; PRIOR FILING DATE: 1998-02-24  
; PRIOR APPLICATION NUMBER: 60/038,253  
; PRIOR FILING DATE: 1997-02-24  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 7  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-057-136-7  
Query Match 100.0%; Score 60; DB 14; Length 60;

Best Local Similarity 100.0%; Pred. No. 7.3e-25;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGTTCGACGGCCCCCTGCTCAGCGGTGTACATCCGCCCGGATACCGACCGGCCCT 60  
Db 1 GGTTCGACGGCCCCCTGCTCAGCGGTGTACATCCGCCCGGATACCGACCGGCCCT 60

RESULT 2  
US-10-406-317-41  
; Sequence 41, Application US/10406317  
; Publication No. US20040019195A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlom, Jeffrey;  
; APPLICANT: Panicali, Dennis  
; TITLE OF INVENTION: A recombinant vector expressing multiple constimulatory  
; TITLE OF INVENTION: molecules and uses thereof  
; FILE REFERENCE: 38163-0189  
; CURRENT APPLICATION NUMBER: US/10/406,317  
; CURRENT FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: US/09/856,988  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: PCT/US99/26866  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/111,582  
; PRIOR FILING DATE: 1998-12-09  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 41  
; LENGTH: 2297  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: VECTOR  
; OTHER INFORMATION: SEQUENCE  
US-10-406-317-41

Query Match 100.0%; Score 60; DB 17; Length 2297;  
Best Local Similarity 100.0%; Pred. No. 4.5e-25;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGTTCGACGGCCCCCTGCTCAGCGGTGTACATCCGCCCGGATACCGACCGGCCCT 60  
Db 586 GGTTCGACGGCCCCCTGCTCAGCGGTGTACATCCGCCCGGATACCGACCGGCCCT 645

RESULT 3  
US-10-369-493-33682  
; Sequence 33682, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 33682  
; LENGTH: 867  
; TYPE: DNA  
; ORGANISM: magnetite-containing magnetic coccus  
US-10-369-493-33682  
Query Match 28.3%; Score 17; DB 17; Length 867;  
Best Local Similarity 100.0%; Pred. No. 5.4;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGTTCGACGGCCCCCT 17  
Db 706 GGTTCGACGGCCCCCT 722

RESULT 4  
US-10-425-115-66540/c  
; Sequence 66540, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 66540  
; LENGTH: 1171  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_160683C.1  
US-10-425-115-66540

Query Match 28.3%; Score 17; DB 20; Length 1171;  
Best Local Similarity 100.0%; Pred. No. 5.2;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CCCCTGCTCAGGTGTA 30  
Db 1048 CCCCTGCTCAGGTGTA 1032

RESULT 5  
US-09-918-995-36727/c  
; Sequence 36727, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 36727  
; LENGTH: 406  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-918-995-36727

Query Match 26.7%; Score 16; DB 10; Length 406;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGCCCCCCTGCTCAC 24  
Db 226 GGCCCCCCTGCTCAC 211

RESULT 6  
US-09-918-995-32117/c  
; Sequence 32117, Application US/09918995  
; Publication No. US20030073623A1

```

; GENERAL INFORMATION:
; APPLICANT: Hysq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32117
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(465)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-32117

```

```

Query Match      26.7%; Score 16; DB 10; Length 465;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      9 GGCCCCCCTGCTCAC 24
      |||||
Db      231 GGCCCCCCTGCTCAC 216

```

# RESULT 7

```

US-10-425-115-92232/c
; Sequence 92232, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 92232
; LENGTH: 769
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_184110C.1
US-10-425-115-92232

```

```

Query Match      26.7%; Score 16; DB 20; Length 769;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      30 AACATCGCCCCGGAT 45
      |||||
Db      592 AACATCGCCCCGGAT 577

```

# RESULT 8

```

US-10-106-698-1517/c
; Sequence 1517, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524

```

```

; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 1517
; LENGTH: 1153
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (495)...(495)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-106-698-1517

```

```

Query Match      26.7%; Score 16; DB 15; Length 1153;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      13 CCCCCTGCTCACGGTG 28
      |||||
Db      162 CCCCCTGCTCACGGTG 147

```

# RESULT 9

```

US-10-369-493-38104/c
; Sequence 38104, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 38104
; LENGTH: 1194
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-38104

```

```

Query Match      26.7%; Score 16; DB 17; Length 1194;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      45 TACCAGACCGGCCCT 60
      |||||
Db      833 TACCAGACCGGCCCT 818

```

# RESULT 10

```

US-10-369-493-35087/c
; Sequence 35087, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493

```



```

; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 35087
; LENGTH: 2064
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-35087

Query Match      26.7%; Score 16; DB 17; Length 2064;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      45 TACCAGACCGGCCCT 60
      |||||
Db      1727 TACCAGACCGGCCCT 1712

RESULT 11
US-10-369-493-38514/c
; Sequence 38514, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 38514
; LENGTH: 2064
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-38514

Query Match      26.7%; Score 16; DB 17; Length 2064;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      45 TACCAGACCGGCCCT 60
      |||||
Db      1727 TACCAGACCGGCCCT 1712

RESULT 12
US-10-369-493-38696/c
; Sequence 38696, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 38696
; LENGTH: 2088
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-38696

Query Match      26.7%; Score 16; DB 17; Length 2088;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      45 TACCAGACCGGCCCT 60
      |||||
Db      1727 TACCAGACCGGCCCT 1712

RESULT 13
US-09-712-363-143/c
; Sequence 143, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712,363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 143
; LENGTH: 3285
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-143

Query Match      26.7%; Score 16; DB 9; Length 3285;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      36 CGCCCCGGATACCAGA 51
      |||||
Db      198 CGCCCCGGATACCAGA 183

RESULT 14
US-09-764-872-812/c
; Sequence 812, Application US/09764872
; Publication No. US20030050231A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA125
; CURRENT APPLICATION NUMBER: US/09/764,872
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 957
; SOFTWARE: PatentIn Ver. 2.0

```



```
; SEQ ID NO 812
; LENGTH: 31718
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-872-812

Query Match      26.7%; Score 16; DB 10; Length 31718;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 GGCCCCCCTGCTCAC 24
      |||||
Db      16570 GGCCCCCCTGCTCAC 16555

RESULT 15
US-09-764-872-813/c
; Sequence 813, Application US/09764872
; Publication No. US20030050231A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA125
; CURRENT APPLICATION NUMBER: US/09/764,872
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 957
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 813
; LENGTH: 31718
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-872-813

Query Match      26.7%; Score 16; DB 10; Length 31718;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 GGCCCCCCTGCTCAC 24
      |||||
Db      16570 GGCCCCCCTGCTCAC 16555
```

Search completed: June 30, 2005, 04:45:59  
Job time : 303.7 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 29, 2005, 19:26:35 ; Search time 51.2 Seconds  
(without alignments)  
1917.512 Million cell updates/sec

Title: US-10-057-136-7  
Perfect score: 60  
Sequence: 1 ggttcgacggccccccctgc.....cggataccagacggccct 60

Scoring table: OLIGO-NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA:  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:  
5: /cgn2\_6/ptodata/1/ina/pctus\_COMB.seq:  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
C 1	16	26.7	10095	3	US-08-822-586-45
C 2	16	26.7	4403765	3	US-09-103-840A-2
C 3	16	26.7	4411529	3	US-09-103-840A-1
4	15	25.0	312	4	US-09-513-999C-13405
5	15	25.0	548	4	US-09-621-976-2414
6	15	25.0	2202	4	US-09-489-039A-5397
7	15	25.0	2975	1	US-08-368-281-1
8	15	25.0	7305	4	US-09-902-540-961
9	15	25.0	11958	3	US-09-134-246-8
10	15	25.0	11958	4	US-09-664-186-8
C 11	15	25.0	36618	4	US-09-949-016-16935
C 12	15	25.0	118067	4	US-09-497-855A-32
13	14	23.3	34	2	US-08-930-274-3
C 14	14	23.3	83	2	US-08-894-228-9
C 15	14	23.3	83	3	US-09-191-521-9
C 16	14	23.3	83	3	US-09-133-321-10
17	14	23.3	84	4	US-09-513-999C-16843
C 18	14	23.3	401	4	US-09-621-976-13452
19	14	23.3	428	4	US-09-902-540-9336
C 20	14	23.3	521	3	US-09-404-879A-115
C 21	14	23.3	521	4	US-09-338-933-115
C 22	14	23.3	521	4	US-09-215-681-115
C 23	14	23.3	521	4	US-09-216-003A-115
C 24	14	23.3	521	4	US-09-667-857-115
25	14	23.3	601	4	US-09-949-016-44522
26	14	23.3	601	4	US-09-949-016-44523
C 27	14	23.3	601	4	US-09-949-016-49677

C 28	14	23.3	601	4	US-09-949-016-49678	Sequence 49678, A
C 29	14	23.3	601	4	US-09-949-016-49679	Sequence 49679, A
C 30	14	23.3	601	4	US-09-949-016-49680	Sequence 49680, A
C 31	14	23.3	601	4	US-09-949-016-63347	Sequence 63347, A
C 32	14	23.3	701	3	US-09-133-321-1	Sequence 1, Appli
C 33	14	23.3	768	3	US-09-328-111-667	Sequence 667, App
34	14	23.3	831	4	US-09-902-540-5839	Sequence 5839, Ap
35	14	23.3	867	4	US-09-902-540-7166	Sequence 7166, Ap
36	14	23.3	894	1	US-08-076-726-10	Sequence 10, Appli
37	14	23.3	894	1	US-08-260-452-3	Sequence 3, Appli
38	14	23.3	894	2	US-08-481-970-3	Sequence 3, Appli
39	14	23.3	894	2	US-08-897-719-3	Sequence 3, Appli
40	14	23.3	894	3	US-09-163-269-3	Sequence 3, Appli
41	14	23.3	894	4	US-09-281-674-3	Sequence 3, Appli
42	14	23.3	932	1	US-08-458-912-1	Sequence 1, Appli
43	14	23.3	932	1	US-08-461-179-1	Sequence 1, Appli
44	14	23.3	932	1	US-08-459-254-1	Sequence 1, Appli
45	14	23.3	932	1	US-08-459-255-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1  
US-08-822-586-45/c  
; Sequence 45, Application US/08822586  
; Patent No. 6015890  
; GENERAL INFORMATION:  
; APPLICANT: WILLIAM R. JACOBS, JR., JAMES M. MUSSEY AND  
; APPLICANT: AMALIO TELENTO  
; TITLE OF INVENTION: AN EMBL OPERON OF MYCOBACTERIA AND  
; TITLE OF INVENTION: MUTANTS THEREOF  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN  
; STREET: 90 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: U.S.A.  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE  
; MEDIUM TYPE: DISKETTE  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/822,586  
; FILING DATE: MARCH 20, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ELIZABETH A. BOGOSIAN  
; REGISTRATION NUMBER: 39,911  
; REFERENCE/DOCKET NUMBER: 96700/437  
; TELEPHONE: (212) 697-5995  
; TELEFAX: (212) 286-0854 or 286-0082  
; TELEX: TWX 710-581-4766  
; INFORMATION FOR SEQ ID NO: 45:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10095  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: Genomic DNA  
; HYPOTHETICAL: NO  
US-08-822-586-45

Query Match 26.7%; Score 16; DB 3; Length 10095;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 CGCCCGGATACAGCA 51  
|||||

Db 3718 CGCCCCGGATACCAGA 3703

## RESULT 2

US-09-103-840A-2/c  
; Sequence 2, Application US/09103840A

; Patent No. 6294328

; GENERAL INFORMATION:

; APPLICANT: FLEISCHMAN, Robert D.

; APPLICANT: WHITE, Owen R.

; APPLICANT: FRASER, Claire M.

; APPLICANT: VENTER, John C.

; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM

; FILE REFERENCE: 24366-20007.00

; CURRENT APPLICATION NUMBER: US/09/103,840A

; CURRENT FILING DATE: 1998-06-24

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 4403765

; TYPE: DNA

; ORGANISM: Mycobacterium tuberculosis

; FEATURE:

; OTHER INFORMATION: CDC 1551

; OTHER INFORMATION: "n" bases at various positions throughout the sequence

; OTHER INFORMATION: represent a, t, c or g

US-09-103-840A-2

Query Match 26.7%; Score 16; DB 3; Length 4403765;

Best Local Similarity 100.0%; Pred. No. 8.4;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 CGCCCCGGATACCAGA 51

|||||

Db 4235673 CGCCCCGGATACCAGA 4235658

## RESULT 3

US-09-103-840A-1/c

; Sequence 1, Application US/09103840A

; Patent No. 6294328

; GENERAL INFORMATION:

; APPLICANT: FLEISCHMAN, Robert D.

; APPLICANT: WHITE, Owen R.

; APPLICANT: FRASER, Claire M.

; APPLICANT: VENTER, John C.

; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM

; FILE REFERENCE: 24366-20007.00

; CURRENT APPLICATION NUMBER: US/09/103,840A

; CURRENT FILING DATE: 1998-06-24

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 4411529

; TYPE: DNA

; ORGANISM: Mycobacterium tuberculosis

; OTHER INFORMATION: H37Rv

US-09-103-840A-1

Query Match

Best Local Similarity 100.0%; Pred. No. 8.4;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 CGCCCCGGATACCAGA 51

|||||

Db 4243427 CGCCCCGGATACCAGA 4243412

## RESULT 4

US-09-513-999C-13405

; Sequence 13405, Application US/09513999C

; Patent No. 6783961

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Duclert, A.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

; Patent No. 6783961

; FILE REFERENCE: 59.US2.REG

; CURRENT APPLICATION NUMBER: US/09/513,999C

; CURRENT FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/122,487

; PRIOR FILING DATE: 1999-02-26

; NUMBER OF SEQ ID NOS: 36681

; SOFTWARE: Patent.pm

; SEQ ID NO 13405

; LENGTH: 312

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: 132

; OTHER INFORMATION: m=a or c

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: 143

; OTHER INFORMATION: m=a or c

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: 145

; OTHER INFORMATION: y=c or t

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: 147

; OTHER INFORMATION: s=g or c

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: 309

; OTHER INFORMATION: y=c or t

US-09-513-999C-13405

Query Match 25.0%; Score 15; DB 4; Length 312;

Best Local Similarity 100.0%; Pred. No. 50;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACGGCCCCCCTGCT 21

|||||

Db 87 ACGGCCCCCCTGCT 101

## RESULT 5

US-09-621-976-2414

; Sequence 2414, Application US/09621976

; Patent No. 6639063

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Jobert, S.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: ESTs and Encoded Human Proteins.

; FILE REFERENCE: GENSET.054PR2

; CURRENT APPLICATION NUMBER: US/09/621,976

; CURRENT FILING DATE: 2000-07-21

; NUMBER OF SEQ ID NOS: 19335

; SOFTWARE: Patent.pm

; SEQ ID NO 2414

; LENGTH: 548

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 95..376

US-09-621-976-2414

Query Match

25.0%; Score 15; DB 4; Length 548;

```
; Best Local Similarity 100.0%; Pred. No. 49;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACGGCCCTGCT 21
Db 113 ACGGCCCTGCT 127

RESULT 6
US-09-489-039A-5397/c
; Sequence 5397, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 5397
; LENGTH: 2202
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-5397

Query Match 25.0%; Score 15; DB 4; Length 2202;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 CCGATACCGACCG 54
Db 1592 CCGATACCGACCG 1578

RESULT 7
US-08-368-281-1
; Sequence 1, Application US/08368281
; Patent No. 5721113
; GENERAL INFORMATION:
; APPLICANT: Libermann, Towia A
; APPLICANT: Oettgen, Joerg P
; APPLICANT: Kunsch, Charles A
; TITLE OF INVENTION: NERF Genes
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/368,281
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096
; TELEFAX: 610-270-5090
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2975 base pairs
; TYPE: nucleic acid
```

```
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-368-281-1

Query Match 25.0%; Score 15; DB 1; Length 2975;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 CTGCTCACGGTGTA 31
Db 70 CTGCTCACGGTGTA 84

RESULT 8
US-09-902-540-961
; Sequence 961, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 961
; LENGTH: 7305
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-961

Query Match 25.0%; Score 15; DB 4; Length 7305;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 TCCGCCCGGATACC 48
Db 4255 TCCGCCCGGATACC 4269

RESULT 9
US-09-134-246-8
; Sequence 8, Application US/09134246B
; Patent No. 6207377
; GENERAL INFORMATION:
; APPLICANT: Wayne, Jay
; APPLICANT: Xu, Shuang-Yong
; TITLE OF INVENTION: Method For Construction Of Thermus-E. coli Shuttle
; TITLE OF INVENTION: Vectors And Identification Of Two Thermus Plasmid
; TITLE OF INVENTION: Replication Origins
; FILE REFERENCE: Thermus Shuttle Vector
; CURRENT APPLICATION NUMBER: US/09/134,246B
; CURRENT FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 11958
; TYPE: DNA
; ORGANISM: Thermus sp.
US-09-134-246-8

Query Match 25.0%; Score 15; DB 3; Length 11958;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CCCCCCTGCTCACGG 26
Db 11709 CCCCCCTGCTCACGG 11723
```

```
RESULT 10
US-09-664-186-8
; Sequence 8, Application US/09664186
; Patent No. 6815537
; GENERAL INFORMATION:
; APPLICANT: Wayne, Jay
; APPLICANT: Xu, Shuang-yong
; TITLE OF INVENTION: Method For Construction Of Thermus-E. coli Shuttle
; TITLE OF INVENTION: Vectors And Identification Of Two Thermus Plasmid
; TITLE OF INVENTION: Replication Origins
; FILE REFERENCE: Thermus Shuttle Vector
; CURRENT APPLICATION NUMBER: US/09/664,186
; CURRENT FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/09/134,246B
; PRIOR FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 11958
; TYPE: DNA
; ORGANISM: Thermus sp.
US-09-664-186-8

Query Match      25.0%; Score 15; DB 4; Length 11958;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CCCCCCTGCTCAGG 26
      |||||
Db 11709 CCCCCCTGCTCAGG 11723

RESULT 11
US-09-949-016-16935/c
; Sequence 16935, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16935
; LENGTH: 36618
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16935

Query Match      25.0%; Score 15; DB 4; Length 36618;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 ATCCGCCCGGATAC 47
      |||||
Db 1566 ATCCGCCCGGATAC 1552

RESULT 12
US-09-497-855A-32/c
; Sequence 32, Application US/09497855A
; Patent No. 6605432
; GENERAL INFORMATION:
```

```
; APPLICANT: Huang, Tim
; TITLE OF INVENTION: HIGH-THROUGHPUT METHODS FOR DETECTING DNA METHYLATION
; FILE REFERENCE: UMO1523
; CURRENT APPLICATION NUMBER: US/09/497,855A
; CURRENT FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/120,592
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: 60/118,760
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 118067
; TYPE: DNA
; ORGANISM: Homo sapiens;
US-09-497-855A-32

Query Match      25.0%; Score 15; DB 4; Length 118067;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CACGGTGTAAACATCC 36
      |||||
Db 81974 CACGGTGTAAACATCC 81960

RESULT 13
US-08-930-274-3
; Sequence 3, Application US/08930274
; Patent No. 5932441
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; APPLICANT:
; TITLE OF INVENTION: VECTORS FOR DIFFERENTIAL EXPRESSION
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., Suite 800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,274
; FILING DATE: September 29, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95302196.1
; FILING DATE: 31-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB 96/00765
; FILING DATE: 29-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-721-8200
; TELEFAX: 202-721-8250
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
```

```
; DESCRIPTION: /desc = "synthetic primer"
US-08-930-274-3
Query Match      23.3%; Score 14; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCGACGGCCCCC 17
   |||||
Db 14 TCGACGGCCCCC 27

RESULT 14
US-08-894-228-9/c
; Sequence 9, Application US/08894228
; Patent No. 5914395
; GENERAL INFORMATION:
; APPLICANT: PAULIN, DENISE
; APPLICANT: LI, ZHEN LIN
; TITLE OF INVENTION: AMPLIFYING SEQUENCES, VECTORS COMPRISING
; TITLE OF INVENTION: THESE SEQUENCES AND THEIR USES IN COMPOSITIONS FOR THE
; TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES IN TRANSFECTED CELLS,
; TITLE OF INVENTION: THERAPEUTIC AND VACCINE APPLICATIONS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,228
; FILING DATE: 12-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR96/00261
; FILING DATE: 16-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95 01937
; FILING DATE: 20-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0660-0123-0X PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 83 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION:
US-08-894-228-9
```

```
Query Match      23.3%; Score 14; DB 2; Length 83;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CCCCCGATACCAGA 51
   |||||
Db 39 CCCCCGATACCAGA 26
```

RESULT 15

```
US-09-191-521-9/c
; Sequence 9, Application US/09191521
; Patent No. 6201115
; GENERAL INFORMATION:
; APPLICANT: PAULIN, DENISE
; APPLICANT: LI, ZHEN LIN
; TITLE OF INVENTION: AMPLIFYING SEQUENCES, VECTORS COMPRISING
; TITLE OF INVENTION: THESE SEQUENCES AND THEIR USES IN COMPOSITIONS FOR THE
; TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES IN TRANSFECTED CELLS,
; TITLE OF INVENTION: THERAPEUTIC AND VACCINE APPLICATIONS
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/191,521
; FILING DATE: 13-NO. 6201115-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,228
; FILING DATE: 12-SEP-1997
; APPLICATION NUMBER: PCT/FR96/00261
; FILING DATE: 16-FEB-1996
; APPLICATION NUMBER: FR 95 01937
; FILING DATE: 20-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 0660-0123-0X PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 83 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-191-521-9

Query Match      23.3%; Score 14; DB 3; Length 83;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CCCCCGATACCAGA 51
   |||||
Db 39 CCCCCGATACCAGA 26

Search completed: June 30, 2005, 04:05:09
Job time : 98.2 secs
```

**THIS PAGE BLANK (USPTO)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 29, 2005, 23:23:45 ; Search time 230.7 Seconds  
(without alignments)  
1625.622 Million cell updates/sec

Title: US-10-057-136-8

Perfect score: 60

Sequence: 1 ggcagcaccgcacccgcgc.....cagacactgcactgcgcca 60

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 6067389 seqs, 3125258755 residues

Word size : 0

Total number of hits satisfying chosen parameters: 12134778

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*
- 18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*
- 19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq:\*
- 20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq:\*
- 21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq:\*
- 22: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*
- 23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq:\*
- 24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*
- 25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*
- 26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	100.0	60	14	US-10-057-136-8
2	42	70.0	60	14	US-10-057-136-9
3	42	70.0	2297	17	US-10-406-317-41
4	19	31.7	1854	17	US-10-282-122A-26264
5	19	31.7	1857	17	US-10-282-122A-28639
6	18	30.0	1605	19	US-10-437-963-41853
7	18	30.0	3644	20	US-10-723-860-7061
					Sequence 8, Appli
					Sequence 9, Appli
					Sequence 41, Appli
					Sequence 26264, A
					Sequence 28639, A
					Sequence 41853, A

Query Match

100.0%; Score 60; DB 14; Length 60;

c	8	17	28.3	351	11	US-09-758-759-164	Sequence 164, App
c	9	17	28.3	1530	19	US-10-437-963-47467	Sequence 47467, A
c	10	17	28.3	2205	15	US-10-156-761-6358	Sequence 6358, Ap
c	11	17	28.3	109519	11	US-09-758-759-1	Sequence 1, Appli
c	12	17	28.3	9025608	15	US-10-156-761-1	Sequence 1, Appli
c	13	16	26.7	889	20	US-10-425-115-24623	Sequence 24623, A
c	14	16	26.7	1365	19	US-10-437-963-18424	Sequence 18424, A
c	15	16	26.7	1643	19	US-10-437-963-45329	Sequence 45329, A
c	16	16	26.7	1676	18	US-10-425-114-13259	Sequence 13259, A
c	17	16	26.7	1957	19	US-10-437-963-18425	Sequence 18425, A
c	18	16	26.7	2214	17	US-10-369-493-44217	Sequence 44217, A
c	19	16	26.7	2352	15	US-10-156-761-4053	Sequence 4053, Ap
c	20	16	26.7	2376	15	US-10-156-761-1892	Sequence 1892, Ap
c	21	16	26.7	2618	14	US-10-175-523-7	Sequence 7, Appli
c	22	16	26.7	2618	14	US-10-175-523-106	Sequence 106, App
c	23	16	26.7	2781	18	US-10-424-599-106970	Sequence 106970,
c	24	16	26.7	7193	14	US-10-071-338-1	Sequence 1, Appli
c	25	16	26.7	7193	15	US-10-288-985-1	Sequence 1, Appli
c	26	16	26.7	7193	15	US-10-289-980-1	Sequence 1, Appli
c	27	16	26.7	7193	16	US-10-214-519-1	Sequence 1, Appli
c	28	16	26.7	7193	18	US-10-138-222-1	Sequence 1, Appli
c	29	16	26.7	30000	11	US-09-980-217-1	Sequence 1, Appli
c	30	16	26.7	2731748	19	US-10-297-465A-1	Sequence 1, Appli
c	31	16	26.7	9025608	15	US-10-156-761-1	Sequence 1, Appli
c	32	15	25.0	216	19	US-10-437-963-68395	Sequence 68395, A
c	33	15	25.0	291	9	US-09-960-352-7658	Sequence 7658, Ap
c	34	15	25.0	313	10	US-09-803-719-1076	Sequence 1076, Ap
c	35	15	25.0	441	17	US-10-369-493-37815	Sequence 37815, A
c	36	15	25.0	442	9	US-09-960-352-12874	Sequence 12874, A
c	37	15	25.0	455	13	US-10-027-632-46136	Sequence 46136, A
c	38	15	25.0	455	17	US-10-027-632-46136	Sequence 46136, A
c	39	15	25.0	540	17	US-10-369-493-38565	Sequence 38565, A
c	40	15	25.0	552	17	US-10-369-493-38134	Sequence 38134, A
c	41	15	25.0	566	16	US-10-029-386-25206	Sequence 25206, A
c	42	15	25.0	596	13	US-10-027-632-132080	Sequence 132080,
c	43	15	25.0	596	17	US-10-027-632-132080	Sequence 132080,
c	44	15	25.0	705	20	US-10-363-345A-23545	Sequence 23545, A
c	45	15	25.0	705	20	US-10-363-345A-23546	Sequence 23546, A

ALIGNMENTS

RESULT 1

US-10-057-136-8  
; Sequence 8, Application US/10057136  
; Publication No. US20030021770A1  
; GENERAL INFORMATION:  
; APPLICANT: SCHLOM, JEFFREY  
; APPLICANT: KANTOR, JUDITH  
; APPLICANT: KUFU, DONALD  
; APPLICANT: PANICALI, DENNIS  
; APPLICANT: GRITZ, LINDA  
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1  
; TITLE OF INVENTION: TUMOR-ASSOCIATED ANTIGEN  
; FILE REFERENCE: 700953/47113C  
; CURRENT APPLICATION NUMBER: US/10/057,136  
; CURRENT FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: 09/366,670  
; PRIOR FILING DATE: 1999-08-03  
; PRIOR APPLICATION NUMBER: PCT/US98/03693  
; PRIOR FILING DATE: 1998-02-24  
; PRIOR APPLICATION NUMBER: 60/038,253  
; PRIOR FILING DATE: 1997-02-24  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-057-136-8

Query Match

100.0%; Score 60; DB 14; Length 60;

```
; OTHER INFORMATION: SEQUENCE
US-10-406-317-41

Query Match      70.0%; Score 42; DB 17; Length 2297;
Best Local Similarity 100.0%; Pred. No. 1.4e-13;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCAGCACCGCACCGCCCGCACACGGGGTCAAAAGCGCGCCAGACACTCGACCTGGGCCA 60
    |||||
Db 1 GGCAGCACCGCACCGCCCGCACACGGGGTCAAAAGCGCGCCAGACACTCGACCTGGGCCA 60

RESULT 2
US-10-057-136-9
; Sequence 9, Application US/10057136
; Publication No. US20030021770A1
; GENERAL INFORMATION:
; APPLICANT: SCHLOM, JEFFREY
; APPLICANT: KANTOR, JUDITH
; APPLICANT: KUPE, DONALD
; APPLICANT: PANICALI, DENNIS
; APPLICANT: GRITZ, LINDA
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1
; FILE REFERENCE: 700953/47113C
; CURRENT APPLICATION NUMBER: US/10/057,136
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 09/366,670
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: PCT/US98/03693
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 60/038,253
; PRIOR FILING DATE: 1997-02-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-057-136-9

Query Match      70.0%; Score 42; DB 14; Length 60;
Best Local Similarity 100.0%; Pred. No. 2.7e-13;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GCACACGGGGTCAAAAGCGCGCCAGACACTCGACCTGGGCCA 60
    |||||
Db 19 GCACACGGGGTCAAAAGCGCGCCAGACACTCGACCTGGGCCA 60

RESULT 3
US-10-406-317-41
; Sequence 41, Application US/10406317
; Publication No. US20040019195A1
; GENERAL INFORMATION:
; APPLICANT: Schlom, Jeffrey;
; APPLICANT: Hodge, James;
; APPLICANT: Panicali, Dennis
; TITLE OF INVENTION: A recombinant vector expressing multiple constimulatory
; FILE REFERENCE: 38163-0189
; CURRENT APPLICATION NUMBER: US/10/406,317
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US/09/856,988
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US99/26866
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/111,582
; PRIOR FILING DATE: 1998-12-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 2297
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VECTOR
```

```
; OTHER INFORMATION: SEQUENCE
US-10-406-317-41

Query Match      70.0%; Score 42; DB 17; Length 2297;
Best Local Similarity 100.0%; Pred. No. 1.4e-13;
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GCACACGGGGTCAAAAGCGCGCCAGACACTCGACCTGGGCCA 60
    |||||
Db 724 GCACACGGGGTCAAAAGCGCGCCAGACACTCGACCTGGGCCA 765

RESULT 4
US-10-282-122A-26264/c
; Sequence 26264, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26264
; LENGTH: 1854
; TYPE: DNA
; ORGANISM: Mycobacterium bovis
US-10-282-122A-26264

Query Match      31.7%; Score 19; DB 17; Length 1854;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCAGCACCGCACCGCCCG 19
    |||||
Db 197 GGCAGCACCGCACCGCCCG 179

RESULT 5
US-10-282-122A-28639/c
```

; Sequence 28639, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 78614

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 28639

; LENGTH: 1857

; TYPE: DNA

; ORGANISM: Mycobacterium tuberculosis

US-10-282-122A-28639

Query Match 31.7%; Score 19; DB 17; Length 1857;

Best Local Similarity 100.0%; Pred. No. 0.64;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCAGCACCGCAGCGCCCG 19

|||||

Db 197 GGCAGCACCGCAGCGCCCG 179

#### RESULT 6

US-10-437-963-41853/c

; Sequence 41853, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 41853

; LENGTH: 1605

; TYPE: DNA

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_4515C.1

US-10-437-963-41853

Query Match 30.0%; Score 18; DB 19; Length 1605;

Best Local Similarity 100.0%; Pred. No. 2.3;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCGCACCGCCGACACG 25

|||||

Db 1241 CCGCACCGCCGACACG 1224

#### RESULT 7

US-10-723-860-7061

; Sequence 7061, Application US/10723860

; Publication No. US20040253606A1

; GENERAL INFORMATION:

; APPLICANT: Aziz, Natasha

; APPLICANT: Ginsburg, Wendy M.

; APPLICANT: Zlotnik, Albert

; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &

; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators

; FILE REFERENCE: 05882.0193.NPUS01

; CURRENT APPLICATION NUMBER: US/10/723,860

; CURRENT FILING DATE: 2003-11-26

; PRIOR APPLICATION NUMBER: 60/429,739

; PRIOR FILING DATE: 2002-11-26

; NUMBER OF SEQ ID NOS: 8393

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 7061

; LENGTH: 3644

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (23)..(23)

; OTHER INFORMATION: n is a, c, g, or t

US-10-723-860-7061

Query Match 30.0%; Score 18; DB 20; Length 3644;

Best Local Similarity 100.0%; Pred. No. 2;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 CAAGCGCGCCAGACACTC 49

|||||

Db 2577 CAAGCGCGCCAGACACTC 2594

#### RESULT 8

US-09-758-759-164/c

; Sequence 164, Application US/09758759

; Publication No. US20040101832A1

; GENERAL INFORMATION:

; APPLICANT: Hosted, Thomas J.

; APPLICANT: Wang, Tim X.

; APPLICANT: Horan, Ann C.

; TITLE OF INVENTION: Evernimicin Biosynthetic Genes

; FILE REFERENCE: ID0983K US

; CURRENT APPLICATION NUMBER: US/09/758,759

; CURRENT FILING DATE: 2001-01-11

; PRIOR APPLICATION NUMBER: US 60/175,751

; PRIOR FILING DATE: 2000-01-12

; NUMBER OF SEQ ID NOS: 204

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 164



```
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match      28.3%; Score 17; DB 15; Length 9025608;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CCGCACCGCCCGCACAC 24
Db      7654924 CCGCACCGCCCGCACAC 7654908

RESULT 13
US-10-425-115-24623/c
; Sequence 24623, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 24623
; LENGTH: 889
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_122463C.1
US-10-425-115-24623

Query Match      26.7%; Score 16; DB 20; Length 889;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 GCACCGCACCGCCGC 20
Db      358 GCACCGCACCGCCGC 343

RESULT 14
US-10-437-963-18424/c
; Sequence 18424, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 18424
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Oryza sativa
```

```
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_23984C.1
US-10-437-963-18424

Query Match      26.7%; Score 16; DB 19; Length 1365;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 CGCACCGCCCGCACAC 24
Db      995 CGCACCGCCCGCACAC 980

RESULT 15
US-10-437-963-45329/c
; Sequence 45329, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 45329
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_48304C.1
US-10-437-963-45329

Query Match      26.7%; Score 16; DB 19; Length 1643;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 CGCACCGCCCGCACAC 24
Db      508 CGCACCGCCCGCACAC 493

Search completed: June 30, 2005, 04:46:42
Job time : 273.7 secs
```

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: June 29, 2005, 19:26:35 ; Search time 51.2 Seconds  
(without alignments)  
1917.512 Million cell updates/sec

Title: US-10-057-136-8  
Perfect score: 60  
Sequence: 1 ggcagcaccgaccgcccgc.....cagacactgcgcca 60

Scoring table: ~~OMIGO\_NUC~~  
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA:  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	31.7	4403765	3	US-09-103-840A-2
2	19	31.7	4411529	3	US-09-103-840A-1
3	16	26.7	1191	4	US-09-489-039A-6256
4	16	26.7	1521	4	US-09-489-039A-5599
5	16	26.7	44377	2	US-08-804-227C-7
6	16	26.7	44377	2	US-08-804-198-1
7	15	25.0	373	4	US-09-270-767-26397
8	15	25.0	750	4	US-09-252-991A-13978
9	15	25.0	867	4	US-09-270-767-10912
10	15	25.0	1038	4	US-09-252-991A-14155
11	15	25.0	2181	3	US-09-780-049-17
12	15	25.0	2182	4	US-09-949-016-5543
13	15	25.0	2793	2	US-08-347-563A-1
14	15	25.0	2793	3	US-08-485-942A-1
15	15	25.0	2793	3	US-08-488-214A-1
16	15	25.0	2793	3	US-08-488-208A-1
17	15	25.0	2793	3	US-08-483-211A-1
18	15	25.0	2793	3	US-08-488-223A-1
19	15	25.0	2793	4	US-08-438-431A-1
20	15	25.0	2793	4	US-08-488-225A-1
21	15	25.0	2793	4	US-09-686-647A-1
22	15	25.0	2966	3	US-09-780-049-3
23	15	25.0	3889	2	US-08-648-298-1
24	15	25.0	5097	4	US-09-902-540-745
25	15	25.0	5336	3	US-09-102-528-11
26	15	25.0	30001	1	US-08-125-468-1
27	15	25.0	30001	2	US-08-474-933-1

C 28	15	25.0	33353	4	US-09-949-016-17285	Sequence 17285, A
C 29	15	25.0	40000	3	US-09-780-049-18	Sequence 18, Appl
C 30	15	25.0	536165	4	US-09-214-808-1	Sequence 1, Appli
C 31	15	25.0	4403765	3	US-09-103-840A-2	Sequence 2, Appli
C 32	15	25.0	4411529	3	US-09-103-840A-1	Sequence 1, Appli
C 33	14	23.3	371	4	US-09-976-594-748	Sequence 748, App
C 34	14	23.3	483	4	US-09-252-991A-468	Sequence 468, App
C 35	14	23.3	513	4	US-09-252-991A-2317	Sequence 2317, Ap
C 36	14	23.3	531	4	US-09-252-991A-5362	Sequence 5362, Ap
C 37	14	23.3	552	4	US-09-252-991A-2597	Sequence 2597, Ap
C 38	14	23.3	586	3	US-09-385-982-469	Sequence 469, App
C 39	14	23.3	597	4	US-09-674-741-3	Sequence 3, Appli
C 40	14	23.3	597	4	US-10-379-010-3	Sequence 3, Appli
C 41	14	23.3	601	4	US-09-949-016-76075	Sequence 76075, A
C 42	14	23.3	601	4	US-09-949-016-78057	Sequence 78057, A
C 43	14	23.3	601	4	US-09-949-016-80723	Sequence 80723, A
C 44	14	23.3	601	4	US-09-949-016-127493	Sequence 127493,
C 45	14	23.3	601	4	US-09-949-016-127494	Sequence 127494,

ALIGNMENTS

RESULT 1

US-09-103-840A-2  
; Sequence 2, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
; TITLE OF INVENTION: TUBERCULOSIS  
; FILE REFERENCE: 24366-20007.00  
; CURRENT APPLICATION NUMBER: US/09/103,840A  
; CURRENT FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 4403765  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
; FEATURE:  
; OTHER INFORMATION: CDC 1551  
; OTHER INFORMATION: "n" bases at various positions throughout the sequence  
; OTHER INFORMATION: represent a, t, c or g  
US-09-103-840A-2

Query Match 31.7%; Score 19; DB 3; Length 4403765;  
Best Local Similarity 100.0%; Pred. No. 0.47;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCAGCACCGCACCGCCCG 19  
Db 3357119 GGCAGCACCGCACCGCCCG 3357137

RESULT 2

US-09-103-840A-1  
; Sequence 1, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
; TITLE OF INVENTION: TUBERCULOSIS  
; FILE REFERENCE: 24366-20007.00  
; CURRENT APPLICATION NUMBER: US/09/103,840A  
; CURRENT FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 2



```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match          31.7%; Score 19; DB 3; Length 4411529;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGCAGCACCGCACC GCCCG 19
      |||||
Db      3362787 GGCAGCACCGCACC GCCCG 3362805

RESULT 3
US-09-489-039A-6256
; Sequence 6256, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 6256
; LENGTH: 1191
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-6256

Query Match          26.7%; Score 16; DB 4; Length 1191;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      31 ACAAGCGCGCCGACACA 46
      |||||
Db      1166 ACAAGCGCGCCGACACA 1181

RESULT 4
US-09-489-039A-5599
; Sequence 5599, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 5599
; LENGTH: 1521
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-5599

Query Match          26.7%; Score 16; DB 4; Length 1521;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      31 ACAAGCGCGCCGACACA 46
      |||||
Db      1 ACAAGCGCGCCGACACA 16
```

```
RESULT 5
US-08-804-227C-7
; Sequence 7, Application US/08804227C
; Patent No. 5876991
; GENERAL INFORMATION:
; APPLICANT: DeHoff, Bradley S.
; APPLICANT: Kuhstoss, Stuart A.
; APPLICANT: Rosteck, Paul R., Jr.
; APPLICANT: Sutton, Kimberly L.
; TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: THOMAS G. PLANT 1501
; STREET: LILLY CORPORATE CENTER
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: ASCII(DOS) Text only
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,227C
; FILING DATE: February 21, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Plant, Thomas, G.
; REGISTRATION NUMBER: 35,784
; REFERENCE/DOCKET NUMBER: X-8231
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-2459
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44377 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 350..14002
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 14046..20036
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 20110..31284
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31329..36071
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 36155..41830
; US-08-804-227C-7

Query Match          26.7%; Score 16; DB 2; Length 44377;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGCAGCACCGCACC GC 16
      |||||
Db      23338 GGCAGCACCGCACC GC 23353

RESULT 6
US-08-804-198-1
; Sequence 1, Application US/08804198
; Patent No. 5945320
; GENERAL INFORMATION:
```



```

; APPLICANT: Burgett, Stanley G.
; APPLICANT: Kuhstoss, Stuart A.
; APPLICANT: Rao, Nagaraja R.
; APPLICANT: Richardson, Mark A.
; APPLICANT: Rosteck, Paul R., Jr.
; TITLE OF INVENTION: PLATENOLIDE SYNTHASE GENE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PAUL R. CANTRELL 1138
; STREET: LILLY CORPORATE CENTER
; CITY: INDIANAPOLIS
; STATE: IN
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh 7.0
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,198
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CANTRELL, PAUL R.
; REGISTRATION NUMBER: 36,470
; REFERENCE/DOCKET NUMBER: P9113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-3885
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 44377 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 350..14002
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 14046..20036
; NAME/KEY: CDS
; LOCATION: 20110..31284
; NAME/KEY: CDS
; LOCATION: 31329..36071
; NAME/KEY: CDS
; LOCATION: 36155..41830
; US-08-804-198-1

Query Match 26.7%; Score 16; DB 2; Length 44377;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCAGCACCGCACCGC 16
Db 23338 GGCAGCACCGCACCGC 23353

RESULT 7
US-09-270-767-26397/c
; Sequence 26397, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10912
; LENGTH: 867
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-10912
Query Match 25.0%; Score 15; DB 4; Length 867;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 CAGACACTCGACCTG 55
Db 321 CAGACACTCGACCTG 307

```

```

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26397
; LENGTH: 373
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-26397

Query Match 25.0%; Score 15; DB 4; Length 373;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 CAGACACTCGACCTG 55
Db 321 CAGACACTCGACCTG 307

RESULT 8
US-09-252-991A-13978/c
; Sequence 13978, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13978
; LENGTH: 750
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13978

Query Match 25.0%; Score 15; DB 4; Length 750;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCAGCACCGCACCGC 16
Db 235 GCAGCACCGCACCGC 221

RESULT 9
US-09-270-767-10912/c
; Sequence 10912, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10912
; LENGTH: 867
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-10912

Query Match 25.0%; Score 15; DB 4; Length 867;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 CAGACACTCGACCTG 55
Db 815 CAGACACTCGACCTG 801

```

RESULT 10  
US-09-252-991A-14155  
; Sequence 14155, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 14155  
; LENGTH: 1038  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-14155

Query Match 25.0%; Score 15; DB 4; Length 1038;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCAGCACCGCACCGC 16  
|||||  
Db 882 GCAGCACCGCACCGC 896

RESULT 11  
US-09-780-049-17/c  
; Sequence 17, Application US/09780049  
; Patent No. 6465250  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Jacqueline Wyatt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN PHOSPHATASE 2 CATALYTIC SUBUNIT  
; TITLE OF INVENTION: EXPRESSION  
; FILE REFERENCE: RTS-0134  
; CURRENT APPLICATION NUMBER: US/09/780,049  
; CURRENT FILING DATE: 2001-02-09  
; NUMBER OF SEQ ID NOS: 96  
; SEQ ID NO 17  
; LENGTH: 2181  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (210)...(1139)  
US-09-780-049-17

Query Match 25.0%; Score 15; DB 3; Length 2181;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CCGCCCGCACACGGG 27  
|||||  
Db 161 CCGCCCGCACACGGG 147

RESULT 12  
US-09-949-016-5543/c  
; Sequence 5543, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 5543  
; LENGTH: 2182  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-5543

Query Match 25.0%; Score 15; DB 4; Length 2182;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CCGCCCGCACACGGG 27  
|||||  
Db 162 CCGCCCGCACACGGG 148

RESULT 13  
US-08-347-563A-1  
; Sequence 1, Application US/08347563A  
; Patent No. 5935810  
; GENERAL INFORMATION:  
; APPLICANT: THE ROCKEFELLER UNIVERSITY  
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC  
; TITLE OF INVENTION: ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauber & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/347,563A  
; FILING DATE: No. 5935810ember 30, 1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/292,345  
; FILING DATE: August 17, 1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201 487-5800  
; TELEFAX: 201 343-1684  
; TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2793 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; DESCRIPTION: Murine ob cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Murine

```
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 57..560
;
US-08-347-563A-1
Query Match      25.0%; Score 15; DB 2; Length 2793;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GCAGCACCACCGC 16
      |||||
Db      2132 GCAGCACCACCGC 2146

RESULT 14
US-08-485-942A-1
; Sequence 1, Application US/08485942A
; Patent No. 6048837
; GENERAL INFORMATION:
; APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA,
; APPLICANT: MARGHERITA MAFFEI, JEFFREY HALAAS, KETAN GAJIWALA, AND STEPHEN K. BURL
; TITLE OF INVENTION: OB POLYPEPTIDE AS MODULATORS OF BODY WEIGHT (AS
; TITLE OF INVENTION: AMENDED)
; NUMBER OF SEQUENCES: 99
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,942A
; FILING DATE: JUNE 7, 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/438,431
; FILING DATE: May 10, 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/347,563
; FILING DATE: No. 6048837ember 30, 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP 2F
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2793 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: Murine ob cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Murine
; FEATURE:
;
```

```
;
; NAME/KEY: CDS
; LOCATION: 57..560
;
US-08-485-942A-1
Query Match      25.0%; Score 15; DB 3; Length 2793;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GCAGCACCACCGC 16
      |||||
Db      2132 GCAGCACCACCGC 2146

RESULT 15
US-08-488-214A-1
; Sequence 1, Application US/08488214A
; Patent No. 6124439
; GENERAL INFORMATION:
; APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA,
; APPLICANT: MARGHERITA MAFFEI, JEFFREY HALAAS, KETAN GAJIWALA, AND STEPHEN K. BURL
; TITLE OF INVENTION: OB POLYPEPTIDE ANTIBODIES AND METHOD OF MAKING
; TITLE OF INVENTION: (AS AMENDED)
; NUMBER OF SEQUENCES: 99
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,214A
; FILING DATE: JUNE 7, 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/438,431
; FILING DATE: May 10, 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/347,563
; FILING DATE: No. 6124439ember 30, 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP 2D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2793 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: Murine ob cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Murine
; FEATURE:
; NAME/KEY: CDS
;
```

```

; LOCATION: 57..560
US-08-488-214A-1
Query Match      25.0%; Score 15; DB 3; Length 2793;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GCAGCACCGCACCGC 16
      |||||
Db      2132 GCAGCACCGCACCGC 2146

Search completed: June 30, 2005, 04:06:20
Job time : 122.2 secs

```

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 29, 2005, 19:26:35 ; Search time 51.2 Seconds  
(without alignments)  
1917.512 Million cell updates/sec

Title: US-10-057-136-9  
Perfect score: 60  
Sequence: 1 ggaagtacgctccacctgc.....cagacactgacctgcgcca 60

Scoring table:  Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA: \*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq: \*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq: \*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq: \*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq: \*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq: \*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	16	26.7	756	4	US-09-902-540-7732
C 2	16	26.7	1191	4	US-09-489-039A-6256
C 3	16	26.7	1521	4	US-09-489-039A-5599
C 4	16	26.7	5262	4	US-09-902-540-766
C 5	15	25.0	144	4	US-09-270-767-28122
C 6	15	25.0	373	4	US-09-270-767-26397
C 7	15	25.0	428	4	US-09-270-767-4535
C 8	15	25.0	428	4	US-09-270-767-19817
C 9	15	25.0	601	4	US-09-949-016-140342
C 10	15	25.0	770	4	US-09-270-767-12366
C 11	15	25.0	867	4	US-09-270-767-10912
C 12	15	25.0	1011	4	US-09-902-540-4174
C 13	15	25.0	1114	4	US-09-902-540-5466
C 14	15	25.0	2843	4	US-09-902-540-5195
C 15	15	25.0	3540	4	US-09-489-039A-6639
C 16	15	25.0	3889	2	US-08-648-298-1
C 17	15	25.0	5336	3	US-09-102-528-11
C 18	15	25.0	13214	4	US-09-949-016-14015
C 19	15	25.0	22301	4	US-09-902-540-1208
C 20	15	25.0	26492	4	US-09-902-540-1234
C 21	15	25.0	29899	4	US-09-902-540-1265
C 22	15	25.0	34199	4	US-09-902-540-1255
C 23	15	25.0	80858	4	US-09-949-016-12659
C 24	15	25.0	80859	4	US-09-949-016-15715
C 25	15	25.0	536165	4	US-09-214-808-1
C 26	14	23.3	263	4	US-09-902-540-5928
C 27	14	23.3	285	4	US-09-513-999C-9020

28	14	23.3	371	4	US-09-976-594-748	Sequence 748, Appl
29	14	23.3	425	1	US-08-357-962-5	Sequence 5, Appli
30	14	23.3	425	1	US-08-878-106-5	Sequence 5, Appli
C 31	14	23.3	483	4	US-09-252-991A-468	Sequence 468, Appl
C 32	14	23.3	513	4	US-09-252-991A-2317	Sequence 2317, Ap
33	14	23.3	531	4	US-09-252-991A-5362	Sequence 5362, Ap
34	14	23.3	536	2	US-08-680-326-3	Sequence 3, Appli
35	14	23.3	552	4	US-09-252-991A-2597	Sequence 2597, Ap
36	14	23.3	586	3	US-09-385-982-469	Sequence 469, Appl
37	14	23.3	601	4	US-09-949-016-78057	Sequence 78057, A
38	14	23.3	601	4	US-09-949-016-127493	Sequence 127493,
39	14	23.3	601	4	US-09-949-016-127494	Sequence 127494,
C 40	14	23.3	601	4	US-09-949-016-152709	Sequence 152709,
41	14	23.3	639	4	US-09-252-991A-5943	Sequence 5943, Ap
42	14	23.3	685	4	US-10-173-082-30	Sequence 30, Appl
43	14	23.3	685	4	US-10-173-082-31	Sequence 31, Appl
44	14	23.3	685	4	US-10-173-082-32	Sequence 32, Appl
45	14	23.3	685	4	US-10-173-082-33	Sequence 33, Appl

ALIGNMENTS

RESULT 1  
US-09-902-540-7732/c  
; Sequence 7732, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 7732  
; LENGTH: 756  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-7732

Query Match 26.7%; Score 16; DB 4; Length 756;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 AGTACCGCTCCACCTG 19  
| | | | | | | | | | | | | | | | | | | | | |  
Db 718 AGTACCGCTCCACCTG 703

RESULT 2  
US-09-489-039A-6256  
; Sequence 6256, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 6256  
; LENGTH: 1191  
; TYPE: DNA  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-6256

```

Query Match      26.7%; Score 16; DB 4; Length 1191;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 ACAAGCGGCCAGACA 46
Db 1166 ACAAGCGGCCAGACA 1181
|||||

RESULT 3
US-09-489-039A-5599
; Sequence 5599, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 5599
; LENGTH: 1521
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-5599

Query Match      26.7%; Score 16; DB 4; Length 1521;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 ACAAGCGGCCAGACA 46
Db 1 ACAAGCGGCCAGACA 16
|||||

RESULT 4
US-09-902-540-766/c
; Sequence 766, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 766
; LENGTH: 5262
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-766

Query Match      26.7%; Score 16; DB 4; Length 5262;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AGTACCGCTCCACCTG 19
Db 2441 AGTACCGCTCCACCTG 2426
|||||

RESULT 5
US-09-270-767-28122
; Sequence 28122, Application US/09270767

```

```

; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28122
; LENGTH: 144
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-28122

Query Match      25.0%; Score 15; DB 4; Length 144;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCGCTCCACCTGCAC 22
Db 7 CCGCTCCACCTGCAC 21
|||||

RESULT 6
US-09-270-767-26397/c
; Sequence 26397, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26397
; LENGTH: 373
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-26397

Query Match      25.0%; Score 15; DB 4; Length 373;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 CAGACACTCGACCTG 55
Db 321 CAGACACTCGACCTG 307
|||||

RESULT 7
US-09-270-767-4535
; Sequence 4535, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4535
; LENGTH: 428
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-4535

Query Match      25.0%; Score 15; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
QY 10 GCTCCACCTGCACAC 24
    |||||
Db 92 GCTCCACCTGCACAC 106

RESULT 8
US-09-270-767-19817
; Sequence 19817, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19817
; LENGTH: 428
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-19817

Query Match 25.0%; Score 15; DB 4; Length 428;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GCTCCACCTGCACAC 24
    |||||
Db 92 GCTCCACCTGCACAC 106

RESULT 9
US-09-949-016-140342
; Sequence 140342, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 140342
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-140342

Query Match 25.0%; Score 15; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 TGCACACGGGGTGCAC 32
    |||||
Db 28 TGCACACGGGGTGCAC 42

RESULT 10
US-09-270-767-12366
; Sequence 12366, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
```

```
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12366
; LENGTH: 770
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-12366

Query Match 25.0%; Score 15; DB 4; Length 770;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCGCTCCACCTGCAC 22
    |||||
Db 7 CCGCTCCACCTGCAC 21

RESULT 11
US-09-270-767-10912/c
; Sequence 10912, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10912
; LENGTH: 867
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-10912

Query Match 25.0%; Score 15; DB 4; Length 867;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 CAGACACTCGACCTG 55
    |||||
Db 815 CAGACACTCGACCTG 801

RESULT 12
US-09-902-540-4174/c
; Sequence 4174, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 4174
; LENGTH: 1011
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-4174

Query Match 25.0%; Score 15; DB 4; Length 1011;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

QY      8 CCGCTCCACCTGCAC 22
      |||||
Db      60 CCGCTCCACCTGCAC 46

RESULT 13
US-09-902-540-5466/c
; Sequence 5466, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 5466
; LENGTH: 1114
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-5466

Query Match      25.0%; Score 15; DB 4; Length 1114;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 AGTACCGCTCCACCT 18
      |||||
Db      878 AGTACCGCTCCACCT 864

RESULT 14
US-09-902-540-5195/c
; Sequence 5195, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 5195
; LENGTH: 2843
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-5195

Query Match      25.0%; Score 15; DB 4; Length 2843;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 GTACCGCTCCACCTG 19
      |||||
Db      2078 GTACCGCTCCACCTG 2064

RESULT 15
US-09-489-039A-6639
; Sequence 6639, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al

```

```

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 6639
; LENGTH: 3540
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-6639

Query Match      25.0%; Score 15; DB 4; Length 3540;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGAAGTACCGCTCCA 15
      |||||
Db      1851 GGAAGTACCGCTCCA 1865

Search completed: June 30, 2005, 04:06:54
Job time : 85.2 secs

```



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 29, 2005, 23:23:45 ; Search time 230.7 Seconds  
(without alignments)  
1625.622 Million cell updates/sec

Title: US-10-057-136-9  
Perfect score: 60  
Sequence: 1 ggaagtagcctccacctgc.....cagacactcgacctgcgcca 60

Scoring table: 1 ggaagtagcctccacctgc.....cagacactcgacctgcgcca 60  
Gapop 60.0 ; Gapext 60.0

Searched: 6067389 seqs, 3125258755 residues

Word size : 0

Total number of hits satisfying chosen parameters: 12134778

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq.\*  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*  
13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*  
14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*  
15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*  
16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*  
17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*  
18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq.\*  
19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq.\*  
20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq.\*  
21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq.\*  
22: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*  
23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq.\*  
24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	60	100.0	60	14	US-10-057-136-9
2	60	100.0	2297	17	US-10-406-317-41
3	42	70.0	60	14	US-10-057-136-8
4	18	30.0	3423	17	US-10-282-122A-40295
5	18	30.0	3644	20	US-10-723-860-7061
6	17	28.3	903	16	US-10-102-239-2
7	17	28.3	1056	16	US-10-102-239-3

8	17	28.3	4451	16	US-10-102-239-1	Sequence 1, Appli
c 9	17	28.3	2256646	19	US-10-470-565-1	Sequence 1, Appli
c 10	16	26.7	1676	18	US-10-425-114-13259	Sequence 13259, A
c 11	16	26.7	2781	18	US-10-424-599-106970	Sequence 106970,
c 12	16	26.7	2731748	19	US-10-297-465A-1	Sequence 1, Appli
c 13	16	26.7	2731748	19	US-10-297-465A-1	Sequence 1, Appli
c 14	15	25.0	277	20	US-10-357-930-7109	Sequence 7109, Ap
c 15	15	25.0	297	19	US-10-437-963-94547	Sequence 94547, A
c 16	15	25.0	313	10	US-09-803-719-1076	Sequence 1076, Ap
c 17	15	25.0	336	17	US-10-242-535A-57308	Sequence 57308, A
c 18	15	25.0	336	18	US-10-085-783A-57308	Sequence 57308, A
c 19	15	25.0	396	9	US-09-983-965-4510	Sequence 4510, Ap
c 20	15	25.0	399	9	US-09-983-965-5245	Sequence 5245, Ap
c 21	15	25.0	410	9	US-09-983-965-4484	Sequence 4484, Ap
c 22	15	25.0	428	9	US-09-983-965-5222	Sequence 5222, Ap
c 23	15	25.0	432	20	US-10-357-930-37078	Sequence 37078, A
c 24	15	25.0	438	20	US-10-425-115-118012	Sequence 118012,
c 25	15	25.0	441	17	US-10-369-493-37815	Sequence 37815, A
c 26	15	25.0	455	13	US-10-027-632-46136	Sequence 46136, A
c 27	15	25.0	455	17	US-10-027-632-46136	Sequence 46136, A
c 28	15	25.0	508	16	US-10-029-386-6481	Sequence 6481, Ap
c 29	15	25.0	508	16	US-10-029-386-11465	Sequence 11465, A
c 30	15	25.0	540	17	US-10-369-493-38565	Sequence 38565, A
c 31	15	25.0	552	17	US-10-369-493-38134	Sequence 38134, A
c 32	15	25.0	620	21	US-10-643-775-638	Sequence 638, App
c 33	15	25.0	622	9	US-09-764-877-1022	Sequence 1022, Ap
c 34	15	25.0	622	17	US-10-242-515-1022	Sequence 1022, Ap
c 35	15	25.0	637	19	US-10-767-701-26630	Sequence 26630, A
c 36	15	25.0	825	20	US-10-425-115-21864	Sequence 21864, A
c 37	15	25.0	975	19	US-10-437-963-90300	Sequence 90300, A
c 38	15	25.0	1040	18	US-10-424-599-106969	Sequence 106969,
c 39	15	25.0	1066	19	US-10-437-963-75417	Sequence 75417, A
c 40	15	25.0	1093	17	US-10-369-493-43217	Sequence 43217, A
c 41	15	25.0	1182	18	US-10-424-599-49049	Sequence 49049, A
c 42	15	25.0	1186	17	US-10-398-221-1748	Sequence 1748, Ap
c 43	15	25.0	1188	17	US-10-282-122A-12241	Sequence 12241, A
c 44	15	25.0	1262	18	US-10-425-114-34238	Sequence 34238, A
c 45	15	25.0	1304	20	US-10-739-930-3223	Sequence 3223, Ap

ALIGNMENTS

RESULT 1  
US-10-057-136-9  
; Sequence 9, Application US/10057136  
; Publication No. US20030021770A1  
; GENERAL INFORMATION:  
; APPLICANT: SCHLOM, JEFFREY  
; APPLICANT: KANTOR, JUDITH  
; APPLICANT: KUFE, DONALD  
; APPLICANT: PANICALI, DENNIS  
; APPLICANT: GRITZ, LINDA  
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1  
; TITLE OF INVENTION: TUMOR-ASSOCIATED ANTIGEN  
; FILE REFERENCE: 700953/47113C  
; CURRENT APPLICATION NUMBER: US/10/057,136  
; CURRENT FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: 09/366,670  
; PRIOR FILING DATE: 1999-08-03  
; PRIOR APPLICATION NUMBER: PCT/US98/03693  
; PRIOR FILING DATE: 1998-02-24  
; PRIOR APPLICATION NUMBER: 60/038,253  
; PRIOR FILING DATE: 1997-02-24  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-057-136-9

Query Match 100.0%; Score 60; DB 14; Length 60;

Best Local Similarity 100.0%; Pred. No. 1.6e-23;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGTACCGCTCCACCTGCACACGGGGTCAAGCGCGCCAGACACTCGACCTGGGCCA 60  
Db 1 GGAAGTACCGCTCCACCTGCACACGGGGTCAAGCGCGCCAGACACTCGACCTGGGCCA 60

RESULT 2  
US-10-406-317-41  
; Sequence 41, Application US/10406317  
; Publication No. US20040019195A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlom, Jeffrey;  
; APPLICANT: Hodge, James;  
; APPLICANT: Panicali, Dennis  
; TITLE OF INVENTION: A recombinant vector expressing multiple constimulatory  
; TITLE OF INVENTION: molecules and uses thereof  
; FILE REFERENCE: 38163-0189  
; CURRENT APPLICATION NUMBER: US/10/406,317  
; CURRENT FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: US/09/856,988  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: PCT/US99/26866  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/111,582  
; PRIOR FILING DATE: 1998-12-09  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 41  
; LENGTH: 2297  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: VECTOR  
; OTHER INFORMATION: SEQUENCE  
US-10-406-317-41

Query Match 100.0%; Score 60; DB 17; Length 2297;  
Best Local Similarity 100.0%; Pred. No. 8.9e-24;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAAGTACCGCTCCACCTGCACACGGGGTCAAGCGCGCCAGACACTCGACCTGGGCCA 60  
Db 706 GGAAGTACCGCTCCACCTGCACACGGGGTCAAGCGCGCCAGACACTCGACCTGGGCCA 765

RESULT 3  
US-10-057-136-8  
; Sequence 8, Application US/10057136  
; Publication No. US20030021770A1  
; GENERAL INFORMATION:  
; APPLICANT: SCHLOM, JEFFREY  
; APPLICANT: KANTOR, JUDITH  
; APPLICANT: KUFE, DONALD  
; APPLICANT: PANICALI, DENNIS  
; APPLICANT: GRITZ, LINDA  
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1  
; TITLE OF INVENTION: TUMOR-ASSOCIATED ANTIGEN  
; FILE REFERENCE: 700953/47113C  
; CURRENT APPLICATION NUMBER: US/10/057,136  
; CURRENT FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: 09/366,670  
; PRIOR FILING DATE: 1999-08-03  
; PRIOR APPLICATION NUMBER: PCT/US98/03693  
; PRIOR FILING DATE: 1998-02-24  
; PRIOR APPLICATION NUMBER: 60/038,253  
; PRIOR FILING DATE: 1997-02-24  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 60  
; TYPE: DNA

; ORGANISM: Homo sapiens  
US-10-057-136-8  
Query Match 70.0%; Score 42; DB 14; Length 60;  
Best Local Similarity 100.0%; Pred. No. 1.7e-13;  
Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GCACACGGGGTCAAGCGCGCCAGACACTCGACCTGGGCCA 60  
Db 19 GCACACGGGGTCAAGCGCGCCAGACACTCGACCTGGGCCA 60

RESULT 4  
US-10-282-122A-40295  
; Sequence 40295, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/230,347  
; PRIOR FILING DATE: 2000-09-09  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625  
; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/267,636  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 78614  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 40295  
; LENGTH: 3423  
; TYPE: DNA  
; ORGANISM: Treponema pallidum  
US-10-282-122A-40295

Query Match 30.0%; Score 18; DB 17; Length 3423;  
Best Local Similarity 100.0%; Pred. No. 2.2;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CGCTCCACCTGCACACGG 26  
Db 1052 CGCTCCACCTGCACACGG 1069

RESULT 5  
US-10-723-860-7061

; Sequence 7061, Application US/10723860  
; Publication No. US20040253606A1  
; GENERAL INFORMATION:  
; APPLICANT: Aziz, Natasha  
; APPLICANT: Ginsburg, Wendy M.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &  
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators  
; FILE REFERENCE: 05882.0193.NPUS01  
; CURRENT APPLICATION NUMBER: US/10/723,860  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: 60/429,739  
; PRIOR FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 8393  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7061  
; LENGTH: 3644  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (23)..(23)  
; OTHER INFORMATION: n is a, c, g, or t  
US-10-723-860-7061

Query Match 30.0%; Score 18; DB 20; Length 3644;  
Best Local Similarity 100.0%; Pred. No. 2.2;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 CAAGCGGCCGACACTC 49  
|||||  
Db 2577 CAAGCGGCCGACACTC 2594

## RESULT 6

US-10-102-239-2  
; Sequence 2, Application US/10102239  
; Publication No. US20030194790A1  
; GENERAL INFORMATION:  
; APPLICANT: Gesellschaft fuer Biotechnologische Forschung  
; APPLICANT: Deckwer, Wolf-Dieter  
; APPLICANT: Mueller, Rolf-Joachim  
; APPLICANT: van den Heuvel, Joop  
; APPLICANT: Kleeberg, Ilona  
; APPLICANT: Widow, Ute  
; TITLE OF INVENTION: DNA-Sequences coding for ester group cleaving enzymes

; FILE REFERENCE: 930008-2068  
; CURRENT APPLICATION NUMBER: US/10/102,239  
; CURRENT FILING DATE: 2002-12-30  
; PRIOR APPLICATION NUMBER: DE 10030529  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: DE 10030529  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: DE 19947286  
; PRIOR FILING DATE: 1999-09-30  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 903  
; TYPE: DNA  
; ORGANISM: Thermomonospora fusca  
US-10-102-239-2

Query Match 28.3%; Score 17; DB 16; Length 903;  
Best Local Similarity 100.0%; Pred. No. 9.8;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AGTACCGCTCCACCTGC 20  
|||||  
Db 881 AGTACCGCTCCACCTGC 897

## RESULT 7

US-10-102-239-3  
; Sequence 3, Application US/10102239  
; Publication No. US20030194790A1  
; GENERAL INFORMATION:  
; APPLICANT: Gesellschaft fuer Biotechnologische Forschung  
; APPLICANT: Deckwer, Wolf-Dieter  
; APPLICANT: Mueller, Rolf-Joachim  
; APPLICANT: van den Heuvel, Joop  
; APPLICANT: Kleeberg, Ilona  
; APPLICANT: Widow, Ute  
; TITLE OF INVENTION: DNA-Sequences coding for ester group cleaving enzymes  
; FILE REFERENCE: 930008-2068  
; CURRENT APPLICATION NUMBER: US/10/102,239  
; CURRENT FILING DATE: 2002-12-30  
; PRIOR APPLICATION NUMBER: DE 10030529  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: DE 10030529  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: DE 19947286  
; PRIOR FILING DATE: 1999-09-30  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 1056  
; TYPE: DNA  
; ORGANISM: Thermomonospora fusca  
US-10-102-239-3

Query Match 28.3%; Score 17; DB 16; Length 1056;  
Best Local Similarity 100.0%; Pred. No. 9.6;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AGTACCGCTCCACCTGC 20  
|||||  
Db 1034 AGTACCGCTCCACCTGC 1050

## RESULT 8

US-10-102-239-1  
; Sequence 1, Application US/10102239  
; Publication No. US20030194790A1  
; GENERAL INFORMATION:  
; APPLICANT: Gesellschaft fuer Biotechnologische Forschung  
; APPLICANT: Deckwer, Wolf-Dieter  
; APPLICANT: Mueller, Rolf-Joachim  
; APPLICANT: van den Heuvel, Joop  
; APPLICANT: Kleeberg, Ilona  
; APPLICANT: Widow, Ute  
; TITLE OF INVENTION: DNA-Sequences coding for ester group cleaving enzymes

; FILE REFERENCE: 930008-2068  
; CURRENT APPLICATION NUMBER: US/10/102,239  
; CURRENT FILING DATE: 2002-12-30  
; PRIOR APPLICATION NUMBER: DE 10030529  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: DE 10030529  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: DE 19947286  
; PRIOR FILING DATE: 1999-09-30  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 4451  
; TYPE: DNA  
; ORGANISM: Thermomonospora fusca  
US-10-102-239-1

Query Match 28.3%; Score 17; DB 16; Length 4451;  
Best Local Similarity 100.0%; Pred. No. 7.7;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AGTACCGCTCCACCTGC 20  
|||||  
Db 2907 AGTACCGCTCCACCTGC 2923

```

RESULT 9
US-10-470-565-1/c
; Sequence 1, Application US/10470565
; Publication No. US20040126870A1
; GENERAL INFORMATION:
; APPLICANT: Societe des Produits Nestle S.A.
; TITLE OF INVENTION: NCC2705 - the genome of a Bifidobacterium
; FILE REFERENCE: 80290/WO
; CURRENT APPLICATION NUMBER: US/10/470,565
; CURRENT FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: EP 01102050.0
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2256646
; TYPE: DNA
; ORGANISM: Bifidobacterium longum
US-10-470-565-1

Query Match      28.3%; Score 17; DB 19; Length 2256646;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 CCACCTGCACACGGGGT 29
      |||||
Db      811934 CCACCTGCACACGGGGT 811918

RESULT 10
US-10-425-114-13259/c
; Sequence 13259, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 13259
; LENGTH: 1676
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: jC-gmle01810054b09_FLI
US-10-425-114-13259

Query Match      26.7%; Score 16; DB 18; Length 1676;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      32 CAAGCGCGCCAGACAC 47
      |||||
Db      1319 CAAGCGCGCCAGACAC 1304

RESULT 11
US-10-424-599-106970/c
; Sequence 106970, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua

```

```

; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 106970
; LENGTH: 2781
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(2781)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_67609C.1
US-10-424-599-106970

Query Match      26.7%; Score 16; DB 18; Length 2781;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      32 CAAGCGCGCCAGACAC 47
      |||||
Db      1838 CAAGCGCGCCAGACAC 1823

RESULT 12
US-10-297-465A-1
; Sequence 1, Application US/10297465A
; Publication No. US20040142413A1
; GENERAL INFORMATION:
; APPLICANT: Simpson, Andrew
; APPLICANT: Reinach, Fernando
; APPLICANT: Setubal, Joao
; APPLICANT: Medianis, Joao
; APPLICANT: Arruda, Paulo
; TITLE OF INVENTION: Isolated Genome of Xylella Fastidiosa and Uses Thereof
; FILE REFERENCE: FAPESP 202 US (10213376)
; CURRENT APPLICATION NUMBER: US/10/297,465A
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: PCT/IB01/01618
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,906
; PRIOR FILING DATE: 2001-06-17
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 2731748
; TYPE: DNA
; ORGANISM: Xylella fastidiosa
US-10-297-465A-1

Query Match      26.7%; Score 16; DB 19; Length 2731748;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      41 CAGACACTCGACCTGC 56
      |||||
Db      1834644 CAGACACTCGACCTGC 1834659

RESULT 13
US-10-297-465A-1/c
; Sequence 1, Application US/10297465A
; Publication No. US20040142413A1
; GENERAL INFORMATION:
; APPLICANT: Simpson, Andrew
; APPLICANT: Reinach, Fernando
; APPLICANT: Setubal, Joao
; APPLICANT: Medianis, Joao
; APPLICANT: Arruda, Paulo

```

; TITLE OF INVENTION: Isolated Genome of Xylella Fastidiosa and Uses Thereof
; FILE REFERENCE: FAPESP 202 US (10213376)
; CURRENT APPLICATION NUMBER: US/10/297,465A
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: PCT/IB01/01618
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,906
; PRIOR FILING DATE: 2001-06-17
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 2731748
; TYPE: DNA
; ORGANISM: Xylella fastidiosa
US-10-297-465A-1

Query Match 26.7%; Score 16; DB 19; Length 2731748;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GCTCCACCTGCACACG 25
|||||
Db 1053172 GCTCCACCTGCACACG 1053157

RESULT 14
US-10-357-930-7109/c
; Sequence 7109, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7109
; LENGTH: 277
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc\_feature
; LOCATION: 90..257
; OTHER INFORMATION: n = A,T,C or G
US-10-357-930-7109

Query Match 25.0%; Score 15; DB 20; Length 277;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 CTGCACACGGGGTCA 31
|||||
Db 188 CTGCACACGGGGTCA 174

RESULT 15
US-10-437-963-94547/c
; Sequence 94547, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 94547
; LENGTH: 297
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_92827C.1
US-10-437-963-94547

Query Match 25.0%; Score 15; DB 19; Length 297;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CCGCTCCACCTGCAC 22
|||||
Db 119 CCGCTCCACCTGCAC 105

Search completed: June 30, 2005, 04:48:28
Job time : 336.7 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 29, 2005, 19:26:35 ; Search time 51.2 seconds  
(without alignments)  
1917.512 Million cell updates/sec

Title: US-10-057-136-10  
Perfect score: 60  
Sequence: 1 gggctgactgccctccggc.....ctgacacaaggccagcccca 60

Scoring table: ~~OMIGO\_NUC~~  
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA: \*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq: \*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq: \*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq: \*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq: \*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq: \*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	18	30.0	77851	4	US-09-949-016-12508
2	18	30.0	77867	4	US-09-949-016-13211
3	18	30.0	77867	4	US-09-949-016-13212
4	18	30.0	77940	4	US-09-949-016-12509
5	18	30.0	107937	4	US-09-949-016-17192
6	17	28.3	131	4	US-09-513-999C-34492
7	17	28.3	601	4	US-09-949-016-45813
8	17	28.3	601	4	US-09-949-016-45814
9	17	28.3	601	4	US-09-949-016-62835
10	17	28.3	601	4	US-09-949-016-62836
11	17	28.3	601	4	US-09-949-016-82326
12	17	28.3	601	4	US-09-949-016-122478
13	17	28.3	601	4	US-09-949-016-122479
14	17	28.3	601	4	US-09-949-016-122594
15	17	28.3	601	4	US-09-949-016-146921
16	17	28.3	601	4	US-09-949-016-146922
17	17	28.3	601	4	US-09-949-016-154399
18	17	28.3	601	4	US-09-949-016-175414
19	17	28.3	601	4	US-09-949-016-187496
20	17	28.3	28555	4	US-09-949-016-13046
21	17	28.3	30002	4	US-09-949-016-15866
22	17	28.3	31390	4	US-09-949-016-15193
23	17	28.3	45755	4	US-09-949-016-15889
24	17	28.3	63804	4	US-09-949-016-15200
25	17	28.3	92505	4	US-09-949-016-14018
26	17	28.3	98362	4	US-09-949-016-14133
27	17	28.3	102884	4	US-09-949-016-17100

28	17	28.3	103792	4	US-09-949-016-13553	Sequence 13553, A
29	17	28.3	103993	4	US-09-949-016-12317	Sequence 12317, A
30	17	28.3	130971	4	US-09-949-016-14205	Sequence 14205, A
31	17	28.3	143644	4	US-09-949-016-15238	Sequence 15238, A
32	17	28.3	144362	4	US-09-949-016-16066	Sequence 16066, A
33	17	28.3	157822	4	US-09-949-016-16723	Sequence 16723, A
34	17	28.3	162450	3	US-09-345-882-1	Sequence 1, Appli
35	17	28.3	187848	4	US-09-949-016-12111	Sequence 12111, A
36	17	28.3	203475	4	US-09-949-016-14516	Sequence 14516, A
37	17	28.3	203475	4	US-09-949-016-14517	Sequence 14517, A
38	17	28.3	203475	4	US-09-949-016-14518	Sequence 14518, A
39	17	28.3	203475	4	US-09-949-016-14519	Sequence 14519, A
40	17	28.3	203475	4	US-09-949-016-17226	Sequence 17226, A
41	17	28.3	203475	4	US-09-949-016-17227	Sequence 17227, A
42	17	28.3	203475	4	US-09-949-016-17228	Sequence 17228, A
43	17	28.3	203475	4	US-09-949-016-17229	Sequence 17229, A
44	16	26.7	145	4	US-09-513-999C-16491	Sequence 16491, A
45	16	26.7	307	4	US-09-313-294A-4743	Sequence 4743, Ap

ALIGNMENTS

RESULT 1  
US-09-949-016-12508  
; Sequence 12508, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12508  
; LENGTH: 77851  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-12508

Query Match 30.0%; Score 18; DB 4; Length 77851;  
Best Local Similarity 100.0%; Pred. No. 2.9;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 ATGGTGTGACCTCAGCTC 40  
|||||  
Db 66930 ATGGTGTGACCTCAGCTC 66947

RESULT 2  
US-09-949-016-13211  
; Sequence 13211, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498



```

; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13211
; LENGTH: 77867
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13211

Query Match          30.0%; Score 18; DB 4; Length 77867;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      23 ATGGTGTGACCTCAGCTC 40
Db      66954 ATGGTGTGACCTCAGCTC 66971

RESULT 3
US-09-949-016-13212
; Sequence 13212, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13212
; LENGTH: 77867
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13212

Query Match          30.0%; Score 18; DB 4; Length 77867;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      23 ATGGTGTGACCTCAGCTC 40
Db      66954 ATGGTGTGACCTCAGCTC 66971

RESULT 4
US-09-949-016-12509
; Sequence 12509, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12509
; LENGTH: 77940

```

```

; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12509

Query Match          30.0%; Score 18; DB 4; Length 77940;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      23 ATGGTGTGACCTCAGCTC 40
Db      67027 ATGGTGTGACCTCAGCTC 67044

RESULT 5
US-09-949-016-17192/c
; Sequence 17192, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17192
; LENGTH: 107937
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(107937)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17192

Query Match          30.0%; Score 18; DB 4; Length 107937;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      23 ATGGTGTGACCTCAGCTC 40
Db      33446 ATGGTGTGACCTCAGCTC 33429

RESULT 6
US-09-513-999C-34492
; Sequence 34492, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 34492
; LENGTH: 131
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-34492

```



Query Match 28.3%; Score 17; DB 4; Length 131;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TGGTGTGACCTCAGCTC 40  
 Db 40 TGGTGTGACCTCAGCTC 56

RESULT 7  
 US-09-949-016-45813/c  
 ; Sequence 45813, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001307  
 ; CURRENT APPLICATION NUMBER: US/09/949,016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 45813  
 ; LENGTH: 601  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 US-09-949-016-45813

Query Match 28.3%; Score 17; DB 4; Length 601;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TGGTGTGACCTCAGCTC 40  
 Db 395 TGGTGTGACCTCAGCTC 379

RESULT 8  
 US-09-949-016-45814/c  
 ; Sequence 45814, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001307  
 ; CURRENT APPLICATION NUMBER: US/09/949,016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 45814  
 ; LENGTH: 601  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 US-09-949-016-45814

Query Match 28.3%; Score 17; DB 4; Length 601;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TGGTGTGACCTCAGCTC 40  
 Db 563 TGGTGTGACCTCAGCTC 547

RESULT 9  
 US-09-949-016-62835/c  
 ; Sequence 62835, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001307  
 ; CURRENT APPLICATION NUMBER: US/09/949,016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 62835  
 ; LENGTH: 601  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 US-09-949-016-62835

Query Match 28.3%; Score 17; DB 4; Length 601;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TGGTGTGACCTCAGCTC 40  
 Db 405 TGGTGTGACCTCAGCTC 389

RESULT 10  
 US-09-949-016-62836/c  
 ; Sequence 62836, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001307  
 ; CURRENT APPLICATION NUMBER: US/09/949,016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 62836  
 ; LENGTH: 601  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 US-09-949-016-62836

Query Match 28.3%; Score 17; DB 4; Length 601;  
 Best Local Similarity 100.0%; Pred. No. 12;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TGGTGTGACCTCAGCTC 40  
 Db 459 TGGTGTGACCTCAGCTC 443

RESULT 11  
US-09-949-016-82326  
; Sequence 82326, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 82326  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-82326

Query Match 28.3%; Score 17; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TGGTGTGACCTCAGCTC 40  
|||||  
Db 184 TGGTGTGACCTCAGCTC 200

RESULT 12  
US-09-949-016-122478/c  
; Sequence 122478, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 122478  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-122478

Query Match 28.3%; Score 17; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TGGTGTGACCTCAGCTC 40  
|||||  
Db 203 TGGTGTGACCTCAGCTC 187

RESULT 13  
US-09-949-016-122479/c  
; Sequence 122479, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 122479  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-122479

Query Match 28.3%; Score 17; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TGGTGTGACCTCAGCTC 40  
|||||  
Db 280 TGGTGTGACCTCAGCTC 264

RESULT 14  
US-09-949-016-122594/c  
; Sequence 122594, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 122594  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-122594

Query Match 28.3%; Score 17; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TGGTGTGACCTCAGCTC 40  
|||||  
Db 502 TGGTGTGACCTCAGCTC 486

RESULT 15  
US-09-949-016-146921  
; Sequence 146921, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 146921  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-146921

Query Match 28.3%; Score 17; DB 4; Length 601;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 42 TGACACAAGGCCAGCCC 58  
||| ||||| ||||| |||||  
Db 544 TGACACAAGGCCAGCCC 560

Search completed: June 30, 2005, 04:08:18  
Job time : 135.2 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 29, 2005, 23:23:45 ; Search time 230.7 Seconds  
(without alignments)  
1625.622 Million cell updates/sec

Title: US-10-057-136-10  
Perfect score: 60  
Sequence: 1 gggctgactgccctccggc.....ctgacacaggccagcccca 60  
Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 6067389 seqs, 3125258755 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 12134778

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:  
9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:  
13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:  
14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:  
15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:  
16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:  
17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:  
18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:  
19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq:  
20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq:  
21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq:  
22: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:  
23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq:  
24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:  
25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:  
26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	60	100.0	60	14	US-10-057-136-10
2	60	100.0	2297	17	US-10-406-317-41
3	19	31.7	25	21	US-10-719-900-598560
4	18	30.0	66025	20	US-10-719-993-6945
5	18	30.0	66025	21	US-10-741-600-17868
6	18	30.0	94330	13	US-10-087-192-1222
7	18	30.0	101193	19	US-10-322-281-468

Query Match 100.0%; Score 60; DB 14; Length 60;

ALIGNMENTS

RESULT 1  
US-10-057-136-10  
; Sequence 10, Application US/10057136  
; Publication No. US20030021770A1  
; GENERAL INFORMATION:  
; APPLICANT: SCHLOM, JEFFREY  
; APPLICANT: KANTOR, JUDITH  
; APPLICANT: KUFU, DONALD  
; APPLICANT: PANICALI, DENNIS  
; APPLICANT: GRITZ, LINDA  
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1  
; TITLE OF INVENTION: TUMOR-ASSOCIATED ANTIGEN  
; FILE REFERENCE: 700953/47113C  
; CURRENT APPLICATION NUMBER: US/10/057,136  
; CURRENT FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: 09/366,670  
; PRIOR FILING DATE: 1999-08-03  
; PRIOR APPLICATION NUMBER: PCT/US98/03693  
; PRIOR FILING DATE: 1998-02-24  
; PRIOR APPLICATION NUMBER: 60/038,253  
; PRIOR FILING DATE: 1997-02-24  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-057-136-10

```

Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTCGACTGCCCTCCGGCGCATGGTGTGACCTCAGCTCTGACACAAAGGCCAGCCCCA 60
Db 1 GGGTCGACTGCCCTCCGGCGCATGGTGTGACCTCAGCTCTGACACAAAGGCCAGCCCCA 60

RESULT 2
US-10-406-317-41
; Sequence 41, Application US/10406317
; Publication No. US20040019195A1
; GENERAL INFORMATION:
; APPLICANT: Schlom, Jeffrey;
; APPLICANT: Panicali, Dennis
; TITLE OF INVENTION: A recombinant vector expressing multiple constimulatory
; TITLE OF INVENTION: molecules and uses thereof
; FILE REFERENCE: 38163-0189
; CURRENT APPLICATION NUMBER: US/10/406,317
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US/09/856,988
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US99/26866
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/111,582
; PRIOR FILING DATE: 1998-12-09
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 2297
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VECTOR
; OTHER INFORMATION: SEQUENCE
US-10-406-317-41

Query Match 100.0%; Score 60; DB 17; Length 2297;
Best Local Similarity 100.0%; Pred. No. 6.1e-24;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTCGACTGCCCTCCGGCGCATGGTGTGACCTCAGCTCTGACACAAAGGCCAGCCCCA 60
Db 766 GGGTCGACTGCCCTCCGGCGCATGGTGTGACCTCAGCTCTGACACAAAGGCCAGCCCCA 825

RESULT 3
US-10-719-900-598560/c
; Sequence 598560, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 598560
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-598560

Query Match 31.7%; Score 19; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 ATGGTGTGACCTCAGCTCC 41
Db 23 ATGGTGTGACCTCAGCTCC 41

```

```

Db 19 ATGGTGTGACCTCAGCTCC 1

RESULT 4
US-10-719-993-6945
; Sequence 6945, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6945
; LENGTH: 66025
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(66025)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-4)
US-10-719-993-6945

Query Match 30.0%; Score 18; DB 20; Length 66025;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 ATGGTGTGACCTCAGCTC 40
Db 13490 ATGGTGTGACCTCAGCTC 13507

RESULT 5
US-10-741-600-17868
; Sequence 17868, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17868
; LENGTH: 66025
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(66025)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-4)
US-10-741-600-17868

Query Match 30.0%; Score 18; DB 21; Length 66025;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 ATGGTGTGACCTCAGCTC 40
Db 13490 ATGGTGTGACCTCAGCTC 13507

RESULT 6
US-10-087-192-1222
; Sequence 1222, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.

```

```

; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 52945200122
; CURRENT APPLICATION NUMBER: US/10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1222
; LENGTH: 94330
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(94330)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-1222

```

```

Query Match      30.0%; Score 18; DB 13; Length 94330;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      23 ATGGTGTGACCTCAGCTC 40
      |||||
Db      75027 ATGGTGTGACCTCAGCTC 75044

```

# RESULT 7

```

US-10-322-281-468
; Sequence 468, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 468
; LENGTH: 101193
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(101193)
; OTHER INFORMATION: n = A,T,C or G
US-10-322-281-468

```

```

Query Match      30.0%; Score 18; DB 19; Length 101193;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      32 CCTCAGCTCCTGACACAA 49
      |||||
Db      59706 CCTCAGCTCCTGACACAA 59723

```

# RESULT 8

```

US-10-719-993-6815
; Sequence 6815, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993

```

```

; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6815
; LENGTH: 1980090
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(1980090)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-719-993-6815

```

```

Query Match      30.0%; Score 18; DB 20; Length 1980090;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      23 ATGGTGTGACCTCAGCTC 40
      |||||
Db      47785 ATGGTGTGACCTCAGCTC 47802

```

# RESULT 9

```

US-10-741-600-17676
; Sequence 17676, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17676
; LENGTH: 1980090
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(1980090)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-741-600-17676

```

```

Query Match      30.0%; Score 18; DB 21; Length 1980090;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      23 ATGGTGTGACCTCAGCTC 40
      |||||
Db      47785 ATGGTGTGACCTCAGCTC 47802

```

# RESULT 10

```

US-10-425-115-177881
; Sequence 177881, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 177881
; LENGTH: 192
; TYPE: DNA
; ORGANISM: Zea mays

```

```

; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_93815C.1
US-10-425-115-177881

Query Match      28.3%; Score 17; DB 20; Length 192;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 TCCTGACACAGGCCAG 55
|||||
Db 107 TCCTGACACAGGCCAG 123

RESULT 11
US-10-719-993-39890
; Sequence 39890, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39890
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-39890

Query Match      28.3%; Score 17; DB 20; Length 201;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TGGTGTGACCTCAGCTC 40
|||||
Db 163 TGGTGTGACCTCAGCTC 179

RESULT 12
US-10-719-993-39891
; Sequence 39891, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39891
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-39891

Query Match      28.3%; Score 17; DB 20; Length 201;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TGGTGTGACCTCAGCTC 40
|||||
Db 10 TGGTGTGACCTCAGCTC 26

RESULT 13
US-10-719-993-40454
; Sequence 40454, Application US/10719993
; Publication No. US20040265849A1

```

```

; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40454
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-40454

Query Match      28.3%; Score 17; DB 20; Length 201;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TGGTGTGACCTCAGCTC 40
|||||
Db 122 TGGTGTGACCTCAGCTC 138

RESULT 14
US-10-357-930-17906/c
; Sequence 17906, Application US/10357930
; Publication No. US20040259086A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Endege, Wilson
; APPLICANT: Monahan, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
; TITLE OF INVENTION: HUMAN PROSTATE CANCER
; FILE REFERENCE: MRI-007BCN
; CURRENT APPLICATION NUMBER: US/10/357,930
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: 09/785,276
; PRIOR FILING DATE: 2003-02-16
; PRIOR APPLICATION NUMBER: 60/183,319
; PRIOR FILING DATE: 2000-02-17
; PRIOR APPLICATION NUMBER: 60/189,862
; PRIOR FILING DATE: 2000-03-16
; PRIOR APPLICATION NUMBER: 60/207,454
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: 60/211,314
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR APPLICATION NUMBER: 60/255,281
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17906
; LENGTH: 314
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-17906

Query Match      28.3%; Score 17; DB 20; Length 314;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TGGTGTGACCTCAGCTC 40
|||||
Db 85 TGGTGTGACCTCAGCTC 69

RESULT 15
US-10-242-535A-33959/c
; Sequence 33959, Application US/10242535A
; Publication No. US20040013663A1

```



```

; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33959
; LENGTH: 318
; TYPE: DNA
; ORGANISM: Human
; US-10-242-535A-33959

Query Match      28.3%; Score 17; DB 17; Length 318;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      24 TGGTGTGACCTCAGCTC 40
      |||||
Db      306 TGGTGTGACCTCAGCTC 290

```

Search completed: June 30, 2005, 04:50:56  
Job time : 378.7 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 29, 2005, 19:26:35 ; Search time 51.2 Seconds  
(without alignments)  
1917.512 Million cell updates/sec

Title: US-10-057-136-11  
Perfect score: 60  
Sequence: 1 ggttaacgacacccagc.....ccgacacccgctccagctccg 60

Scoring table: ~~40MGO\_NUC~~  
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA: \*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq: \*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq: \*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq: \*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq: \*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq: \*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	30.0	4594	4	US-09-112-580-3
2	18	30.0	48471	4	US-09-949-016-16416
3	16	26.7	492	4	US-09-270-767-2029
4	16	26.7	492	4	US-09-270-767-17311
5	16	26.7	1473	4	US-09-902-540-5372
6	16	26.7	34662	4	US-09-902-540-1261
7	15	25.0	68	4	US-09-513-999C-18503
8	15	25.0	284	4	US-09-513-999C-35189
9	15	25.0	495	4	US-09-270-767-2040
10	15	25.0	495	4	US-09-270-767-17322
11	15	25.0	601	4	US-09-949-016-131295
12	15	25.0	601	4	US-09-949-016-131297
13	15	25.0	1327	4	US-09-270-957-9
14	15	25.0	1386	4	US-09-489-039A-5005
15	15	25.0	1440	4	US-09-270-767-12289
16	15	25.0	1614	4	US-09-902-540-8389
17	15	25.0	2190	4	US-09-270-767-12310
18	15	25.0	2503	4	US-09-602-777A-277
19	15	25.0	7186	4	US-09-902-540-879
20	15	25.0	20063	4	US-09-949-016-14176
21	15	25.0	20520	4	US-09-949-016-14394
22	15	25.0	51508	4	US-09-949-016-16681
23	15	25.0	77536	4	US-09-410-551B-1
24	15	25.0	77536	4	US-09-410-551B-1
25	15	25.0	77536	4	US-09-940-316B-1
26	15	25.0	77536	4	US-09-940-316B-1
27	15	25.0	199945	4	US-09-949-016-15436

28	15	25.0	4403765	3	US-09-103-840A-2	Sequence 2, Appli
29	15	25.0	4411529	3	US-09-103-840A-1	Sequence 1, Appli
30	14	23.3	20	3	US-09-226-568-21	Sequence 21, Appl
31	14	23.3	25	4	US-09-396-196G-80372	Sequence 80372, A
32	14	23.3	25	4	US-09-396-196G-80383	Sequence 80383, A
33	14	23.3	25	4	US-09-396-196G-101052	Sequence 101052,
34	14	23.3	25	4	US-09-396-196G-101053	Sequence 101053,
35	14	23.3	25	4	US-09-396-196G-101054	Sequence 101054,
36	14	23.3	123	1	US-08-299-498A-14	Sequence 14, Appl
37	14	23.3	123	5	PCT-US95-10813-14	Sequence 14, Appl
38	14	23.3	387	4	US-09-513-999C-35884	Sequence 35884, A
39	14	23.3	416	4	US-09-544-398B-45	Sequence 45, Appl
40	14	23.3	416	4	US-09-543-771B-45	Sequence 45, Appl
41	14	23.3	435	4	US-09-621-976-698	Sequence 698, App
42	14	23.3	459	4	US-09-252-991A-5249	Sequence 5249, Ap
43	14	23.3	488	4	US-09-902-540-3353	Sequence 3353, Ap
44	14	23.3	495	4	US-09-312-283C-361	Sequence 361, App
45	14	23.3	525	4	US-09-902-540-8850	Sequence 8850, Ap

ALIGNMENTS

RESULT 1  
US-09-112-580-3  
; Sequence 3, Application US/09112580  
; Patent No. 6610539  
; GENERAL INFORMATION:  
; APPLICANT: WRIGHT, Jim A.  
; APPLICANT: YOUNG, Aiping  
; APPLICANT: DUGOURD, Dominique  
; TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE SEQUENCES AS INHIBITORS OF  
; TITLE OF INVENTION: MICROORGANISMS  
; FILE REFERENCE: 032396-016  
; CURRENT APPLICATION NUMBER: US/09/112,580  
; CURRENT FILING DATE: 1998-07-09  
; EARLIER APPLICATION NUMBER: US 60/052,160  
; EARLIER FILING DATE: 1997-07-10  
; NUMBER OF SEQ ID NOS: 265  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 4594  
; TYPE: DNA  
; ORGANISM: Salmonella typhimurium  
US-09-112-580-3

Query Match 30.0%; Score 18; DB 4; Length 4594;  
Best Local Similarity 100.0%; Pred. No. 2.7;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 32 CGTCTGCACCCGACACCC 49  
DB 121 CGTCTGCACCCGACACCC 138

RESULT 2  
US-09-949-016-16416  
; Sequence 16416, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 16416  
; LENGTH: 48471  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-16416

Query Match 30.0%; Score 18; DB 4; Length 48471;  
Best Local Similarity 100.0%; Pred. No. 2.6;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 CGTCTGCACCGACACCC 49  
|||  
Db 31062 CGTCTGCACCGACACCC 31079

RESULT 3  
US-09-270-767-2029/c  
; Sequence 2029, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2029  
; LENGTH: 492  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-2029

Query Match 26.7%; Score 16; DB 4; Length 492;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AACGGCACCTCCAGCA 21  
|||  
Db 350 AACGGCACCTCCAGCA 335

RESULT 4  
US-09-270-767-17311/c  
; Sequence 17311, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17311  
; LENGTH: 492  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-17311

Query Match 26.7%; Score 16; DB 4; Length 492;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AACGGCACCTCCAGCA 21  
|||  
Db 350 AACGGCACCTCCAGCA 335

RESULT 5  
US-09-902-540-5372/c  
; Sequence 5372, Application US/09902540

; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 5372  
; LENGTH: 1473  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-5372

Query Match 26.7%; Score 16; DB 4; Length 1473;  
Best Local Similarity 100.0%; Pred. No. 31;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAACGGCACCTCCAGC 20  
|||  
Db 1380 CAACGGCACCTCCAGC 1365

RESULT 6  
US-09-902-540-1261  
; Sequence 1261, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 1261  
; LENGTH: 34662  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
US-09-902-540-1261

Query Match 26.7%; Score 16; DB 4; Length 34662;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CAACGGCACCTCCAGC 20  
|||  
Db 30265 CAACGGCACCTCCAGC 30280

RESULT 7  
US-09-513-999C-18503/c  
; Sequence 18503, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487

```
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 18503
; LENGTH: 68
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 7
; OTHER INFORMATION: s=g or c
US-09-513-999C-18503

Query Match          25.0%; Score 15; DB 4; Length 68;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GCACCTCCAGCACAC 24
Db 64 GCACCTCCAGCACAC 50

RESULT 8
US-09-513-999C-35189/c
; Sequence 35189, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 35189
; LENGTH: 284
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 275
; OTHER INFORMATION: y=c or t
US-09-513-999C-35189

Query Match          25.0%; Score 15; DB 4; Length 284;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CCTCCAGCACACGGA 27
Db 201 CCTCCAGCACACGGA 187

RESULT 9
US-09-270-767-2040
; Sequence 2040, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2040
; LENGTH: 495
; TYPE: DNA
```

```
; ORGANISM: Drosophila melanogaster
US-09-270-767-2040

Query Match          25.0%; Score 15; DB 4; Length 495;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACGGCACCTCCAGCA 21
Db 83 ACGGCACCTCCAGCA 97

RESULT 10
US-09-270-767-17322
; Sequence 17322, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17322
; LENGTH: 495
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-17322

Query Match          25.0%; Score 15; DB 4; Length 495;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACGGCACCTCCAGCA 21
Db 83 ACGGCACCTCCAGCA 97

RESULT 11
US-09-949-016-131295
; Sequence 131295, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE; METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 131295
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-131295

Query Match          25.0%; Score 15; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 CGTCTGCACCCGACA 46
Db 228 CGTCTGCACCCGACA 242
```

```

RESULT 12
US-09-949-016-131297
; Sequence 131297, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 131297
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-131297

Query Match      25.0%; Score 15; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 CGTCTGCACCCGACA 46
    |||||
Db 397 CGTCTGCACCCGACA 411

RESULT 13
US-09-270-957-9
; Sequence 9, Application US/09270957
; Patent No. 6641996
; GENERAL INFORMATION:
; APPLICANT: Richard A. Jefferson and Jorge E. Mayer
; TITLE OF INVENTION: MICROBIAL -GLUCURONIDASE GENES, GENE
; TITLE OF INVENTION: PRODUCTS, AND USES THEREOF
; FILE REFERENCE: 190106.405C1
; CURRENT APPLICATION NUMBER: US/09/270,957
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1327
; TYPE: DNA
; ORGANISM: Enterobacter sp. / Salmonella sp.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(1327)
; OTHER INFORMATION: n = A,T,C or G
US-09-270-957-9

Query Match      25.0%; Score 15; DB 4; Length 1327;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 CCGACACCCCGTCCA 54
    |||||
Db 731 CCGACACCCCGTCCA 745

RESULT 14
US-09-489-039A-5005/c
; Sequence 5005, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

```

```

; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 5005
; LENGTH: 1386
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-5005

Query Match      25.0%; Score 15; DB 4; Length 1386;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AACGGCACCTCCAGC 20
    |||||
Db 1118 AACGGCACCTCCAGC 1104

RESULT 15
US-09-270-767-12289/c
; Sequence 12289, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12289
; LENGTH: 1440
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-12289

Query Match      25.0%; Score 15; DB 4; Length 1440;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGGCACCTCCAGCAC 22
    |||||
Db 586 CGGCACCTCCAGCAC 572

Search completed: June 30, 2005, 04:09:22
Job time : 115.2 secs

```



Best Local Similarity 100.0%; Pred. No. 2.8e-24;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCAACGGCACTCCAGCACACGAGTACGCTGTGCACCCGACACCCGTCAGCTCCG 60  
Db 1 GGTCAACGGCACTCCAGCACACGAGTACGCTGTGCACCCGACACCCGTCAGCTCCG 60

RESULT 2  
US-10-406-317-41  
; Sequence 41, Application US/10406317  
; Publication No. US20040019195A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlom, Jeffrey;  
; APPLICANT: Hodge, James;  
; APPLICANT: Panicali, Dennis  
; TITLE OF INVENTION: A recombinant vector expressing multiple constitutulatory  
; TITLE OF INVENTION: molecules and uses thereof  
; FILE REFERENCE: 38163-0189  
; CURRENT APPLICATION NUMBER: US/10/406,317  
; CURRENT FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: US/09/856,988  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: PCT/US99/26866  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/111,582  
; PRIOR FILING DATE: 1998-12-09  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 41  
; LENGTH: 2297  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: VECTOR  
; OTHER INFORMATION: SEQUENCE  
US-10-406-317-41

Query Match 100.0%; Score 60; DB 17; Length 2297;  
Best Local Similarity 100.0%; Pred. No. 1.7e-24;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCAACGGCACTCCAGCACACGAGTACGCTGTGCACCCGACACCCGTCAGCTCCG 60  
Db 826 GGTCAACGGCACTCCAGCACACGAGTACGCTGTGCACCCGACACCCGTCAGCTCCG 885

RESULT 3  
US-10-108-260A-909/c  
; Sequence 909, Application US/10108260A  
; Publication No. US20040005560A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA  
; FILE REFERENCE: H1-A0106  
; CURRENT APPLICATION NUMBER: US/10/108,260A  
; CURRENT FILING DATE: 2002-03-27  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 909  
; LENGTH: 2589  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-108-260A-909

Query Match 30.0%; Score 18; DB 17; Length 2589;  
Best Local Similarity 100.0%; Pred. No. 1.6;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AACGGCACCTCCAGCACCA 23  
Db 1533 AACGGCACCTCCAGCACCA 1516

RESULT 4  
US-10-242-355-1086/c  
; Sequence 1086, Application US/10242355  
; Publication No. US20030235831A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC003C1  
; CURRENT APPLICATION NUMBER: US/10/242,355  
; CURRENT FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: 09/764,897  
; PRIOR FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: 60/179,065  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: 60/180,628  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: 60/214,886  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/217,487  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/225,758  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/220,963  
; PRIOR FILING DATE: 2000-07-26  
; PRIOR APPLICATION NUMBER: 60/217,496  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/225,447  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/218,290  
; PRIOR FILING DATE: 2000-07-14  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 1267  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1086  
; LENGTH: 12614  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-242-355-1086

Query Match 30.0%; Score 18; DB 17; Length 12614;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AACGGCACCTCCAGCACCA 23  
Db 2885 AACGGCACCTCCAGCACCA 2868

RESULT 5  
US-10-425-114-2162  
; Sequence 2162, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 2162  
; LENGTH: 738  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700205315\_FLI  
US-10-425-114-2162



```
Query Match      28.3%; Score 17; DB 18; Length 738;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GTTCAACGGCACCTCCA 18
Db      58 GTTCAACGGCACCTCCA 74

RESULT 6
US-10-425-114-33665
; Sequence 33665, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 33665
; LENGTH: 2337
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17156D10_FLI
US-10-425-114-33665

Query Match      28.3%; Score 17; DB 18; Length 2337;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GTTCAACGGCACCTCCA 18
Db      1657 GTTCAACGGCACCTCCA 1673

RESULT 7
US-10-425-115-133325
; Sequence 133325, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 133325
; LENGTH: 2420
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_53081C.1
US-10-425-115-133325

Query Match      28.3%; Score 17; DB 20; Length 2420;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GTTCAACGGCACCTCCA 18
Db      1657 GTTCAACGGCACCTCCA 1673
```

```
Db      1657 GTTCAACGGCACCTCCA 1673

RESULT 8
US-10-425-114-32585
; Sequence 32585, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 32585
; LENGTH: 2442
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17006E01_FLI
US-10-425-114-32585

Query Match      28.3%; Score 17; DB 18; Length 2442;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GTTCAACGGCACCTCCA 18
Db      1762 GTTCAACGGCACCTCCA 1778

RESULT 9
US-10-425-115-133324
; Sequence 133324, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 133324
; LENGTH: 2442
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_53080C.1
US-10-425-115-133324

Query Match      28.3%; Score 17; DB 20; Length 2442;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GTTCAACGGCACCTCCA 18
Db      1762 GTTCAACGGCACCTCCA 1778

RESULT 10
US-10-168-663-18/c
; Sequence 18, Application US/10168663
; Publication No. US20040086962A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Plant Bioscience Limited
; APPLICANT: Chater, Keith F
; APPLICANT: Bruton, Celia J
; APPLICANT: O'Rourke, Sean J
; APPLICANT: Wietzorrek, Andreas W
; TITLE OF INVENTION: Methods and Materials Relating to Gene Expression
; FILE REFERENCE: 0380-P02909US0
; CURRENT APPLICATION NUMBER: US/10/168,663
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/GB00/04972
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: GB 9930477.6
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 9521
; TYPE: DNA
; ORGANISM: Streptomyces coelicolor
US-10-168-663-18

Query Match      28.3%; Score 17; DB 18; Length 9521;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 CAACGGCACCTCCAGCA 21
      |||||
Db      5271 CAACGGCACCTCCAGCA 5255

RESULT 11
US-10-168-663-19
; Sequence 19, Application US/10168663
; Publication No. US20040086962A1
; GENERAL INFORMATION:
; APPLICANT: Plant Bioscience Limited
; APPLICANT: Chater, Keith F
; APPLICANT: Bruton, Celia J
; APPLICANT: O'Rourke, Sean J
; APPLICANT: Wietzorrek, Andreas W
; TITLE OF INVENTION: Methods and Materials Relating to Gene Expression
; FILE REFERENCE: 0380-P02909US0
; CURRENT APPLICATION NUMBER: US/10/168,663
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/GB00/04972
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: GB 9930477.6
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 9521
; TYPE: DNA
; ORGANISM: Streptomyces coelicolor
US-10-168-663-19

Query Match      28.3%; Score 17; DB 18; Length 9521;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 CAACGGCACCTCCAGCA 21
      |||||
Db      4251 CAACGGCACCTCCAGCA 4267

RESULT 12
US-10-060-793-35
; Sequence 35, Application US/10060793
; Publication No. US20030196217A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip

```

```

; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: DESATURASE GENES, ENZYMES ENCODED
; TITLE OF INVENTION: THEREBY, AND USES THEREOF
; FILE REFERENCE: 6884.US.O1
; CURRENT APPLICATION NUMBER: US/10/060,793
; CURRENT FILING DATE: 2002-06-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Forward Primer R0975
US-10-060-793-35

Query Match      26.7%; Score 16; DB 16; Length 29;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 ACCTCCAGCACACGGA 27
      |||||
Db      6 ACCTCCAGCACACGGA 21

RESULT 13
US-10-911-838-71
; Sequence 71, Application US/10911838
; Publication No. US20050069869A1
; GENERAL INFORMATION:
; APPLICANT: AMBROSINO, Donna
; APPLICANT: HERNANDEZ, Hector
; APPLICANT: GREENOUGH, Thomas
; APPLICANT: LUZURIAGA, Katherine
; APPLICANT: SOMASUNDARAN, Mohan
; APPLICANT: BABCOCK, Gregory J.
; APPLICANT: THOMAS, JR., William D.
; APPLICANT: SULLIVAN, John
; TITLE OF INVENTION: SARS NUCLEIC ACIDS, PROTEINS, ANTIBODIES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: MJ1-002
; CURRENT APPLICATION NUMBER: US/10/911,838
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: US 60/565595
; PRIOR FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: US 60/545670
; PRIOR FILING DATE: 2004-02-18
; PRIOR APPLICATION NUMBER: US 60/510251
; PRIOR FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US 60/492529
; PRIOR FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 70
; TYPE: DNA
; ORGANISM: SARS-Associated Coronavirus
US-10-911-838-71

Query Match      26.7%; Score 16; DB 21; Length 70;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GTTCAACGGCACCTCC 17
      |||||
Db      1 GTTCAACGGCACCTCC 16

RESULT 14
US-10-911-838-81/c
; Sequence 81, Application US/10911838
; Publication No. US20050069869A1

```

Search completed: June 30, 2005, 04:52:48  
Job time : 342.7 secs

```
; GENERAL INFORMATION:
; APPLICANT: AMBROSINO, Donna
; APPLICANT: HERNANDEZ, Hector
; APPLICANT: GREENOUGH, Thomas
; APPLICANT: LUZURIAGA, Katherine
; APPLICANT: SOMASUNDARAN, Mohan
; APPLICANT: BABCOCK, Gregory J.
; APPLICANT: THOMAS, JR., William D.
; APPLICANT: SULLIVAN, John
; TITLE OF INVENTION: SARS NUCLEIC ACIDS, PROTEINS, ANTIBODIES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: MJ1-002
; CURRENT APPLICATION NUMBER: US/10/911,838
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: US 60/565595
; PRIOR FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: US 60/545670
; PRIOR FILING DATE: 2004-02-18
; PRIOR APPLICATION NUMBER: US 60/510251
; PRIOR FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US 60/492529
; PRIOR FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 70
; TYPE: DNA
; ORGANISM: SARS-Associated Coronavirus
US-10-911-838-81
```

```
Query Match      26.7%; Score 16; DB 21; Length 70;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      2 GTTCAACGGCACCTCC 17
      |||||
Db      35 GTTCAACGGCACCTCC 20
```

```
RESULT 15
US-09-560-863-437/c
; Sequence 437, Application US/09560863
; Patent No. US20020110809A1
; GENERAL INFORMATION:
; APPLICANT: Nehls, Michael C.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20020110809A1 Human Polynucleotides and the
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: LEX-0018-USA
; CURRENT APPLICATION NUMBER: US/09/560,863
; CURRENT FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/132,408
; PRIOR FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 1008
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 437
; LENGTH: 406
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(406)
; OTHER INFORMATION: n = A,T,C or G
US-09-560-863-437
```

```
Query Match      26.7%; Score 16; DB 9; Length 406;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      2 GTTCAACGGCACCTCC 17
      |||||
Db      208 GTTCAACGGCACCTCC 193
```

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 29, 2005, 19:26:35 ; Search time 51.2 Seconds  
(without alignments)  
1917.512 Million cell updates/sec

Title: US-10-057-136-12  
Perfect score: 60  
Sequence: 1 ggtagtacagcgccaccgcg.....cggatacgagaccggcgccct 60

Scoring table: ~~GenCore NUC~~  
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA:\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCITUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	28.3	2208	4	US-09-489-039A-2376
2	16	26.7	240	4	US-09-252-991A-9393
3	16	26.7	837	4	US-09-252-991A-9468
4	16	26.7	1005	4	US-09-976-594-209
5	16	26.7	1371	4	US-09-252-991A-9440
6	16	26.7	36075	4	US-09-949-016-16571
7	16	26.7	36075	4	US-09-949-016-16572
8	16	26.7	36625	4	US-09-949-016-12788
9	16	26.7	37133	4	US-09-949-016-16569
10	16	26.7	37133	4	US-09-949-016-16570
11	15	25.0	318	3	US-09-060-756-171
12	15	25.0	318	4	US-09-670-314-171
13	15	25.0	350	3	US-09-060-756-397
14	15	25.0	350	4	US-09-670-314-137
15	15	25.0	357	3	US-09-060-756-137
16	15	25.0	357	4	US-09-670-314-137
17	15	25.0	448	3	US-09-060-756-64
18	15	25.0	448	4	US-09-670-314-64
19	15	25.0	465	4	US-09-270-767-9372
20	15	25.0	465	4	US-09-270-767-24654
21	15	25.0	639	4	US-09-252-991A-14012
22	15	25.0	678	4	US-09-252-991A-14466
23	15	25.0	999	3	US-08-818-112-52
24	15	25.0	999	3	US-08-818-111-52
25	15	25.0	999	3	US-09-056-556-52
26	15	25.0	999	3	US-09-072-967-52
27	15	25.0	999	4	US-09-072-967-52

28	15	25.0	1122	4	US-09-510-031A-1	Sequence 1, Appli
29	15	25.0	1269	4	US-09-252-991A-14054	Sequence 14054, A
30	15	25.0	1323	4	US-09-252-991A-14169	Sequence 14169, A
31	15	25.0	1374	4	US-09-252-991A-15159	Sequence 15159, A
32	15	25.0	1656	4	US-09-902-540-6531	Sequence 6531, Ap
33	15	25.0	1782	4	US-09-252-991A-14102	Sequence 14102, A
34	15	25.0	1872	4	US-09-252-991A-14602	Sequence 14602, A
35	15	25.0	1896	3	US-09-232-200-31	Sequence 31, Appl
36	15	25.0	1896	3	US-09-232-197-31	Sequence 31, Appl
37	15	25.0	1896	3	US-09-232-201-31	Sequence 31, Appl
38	15	25.0	1896	4	US-09-232-195-31	Sequence 31, Appl
39	15	25.0	1962	3	US-09-072-596-349	Sequence 349, App
40	15	25.0	1962	4	US-09-072-967-354	Sequence 354, App
41	15	25.0	2061	1	US-08-382-184-1	Sequence 1, Appli
42	15	25.0	2061	2	US-08-641-356-1	Sequence 1, Appli
43	15	25.0	2061	3	US-09-132-528-1	Sequence 1, Appli
44	15	25.0	2061	3	US-08-875-494-1	Sequence 1, Appli
45	15	25.0	2061	3	US-09-599-366-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1  
US-09-489-039A-2376  
; Sequence 2376, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 2376  
; LENGTH: 2208  
; TYPE: DNA  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-2376

Query Match 28.3%; Score 17; DB 4; Length 2208;  
Best Local Similarity 100.0%; Pred. No. 3.6;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 AGTACAGCGCCACCCGC 20  
|||||  
DB 2051 AGTACAGCGCCACCCGC 2067

RESULT 2  
US-09-252-991A-9393  
; Sequence 9393, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 9393  
; LENGTH: 240  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-9393

Query Match 26.7%; Score 16; DB 4; Length 240;  
 Best Local Similarity 100.0%; Pred. No. 15;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 CGAGCGCTCCGGATAC 47  
 |||||  
 Db 122 CGAGCGCTCCGGATAC 137

RESULT 3  
 US-09-252-991A-9468/c  
 ; Sequence 9468, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 107196.136  
 ; CURRENT APPLICATION NUMBER: US/09/252,991A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO 9468  
 ; LENGTH: 837  
 ; TYPE: DNA  
 ; ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-9468

Query Match 26.7%; Score 16; DB 4; Length 837;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 CGAGCGCTCCGGATAC 47  
 |||||  
 Db 712 CGAGCGCTCCGGATAC 697

RESULT 4  
 US-09-976-594-209  
 ; Sequence 209, Application US/09976594  
 ; Patent No. 6673549  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Buchbinder, Jenny  
 ; APPLICANT: Furness, Michael  
 ; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS  
 ; FILE REFERENCE: PA-0041 US  
 ; CURRENT APPLICATION NUMBER: US/09/976,594  
 ; CURRENT FILING DATE: 2001-10-12  
 ; PRIOR APPLICATION NUMBER: 60/240,409  
 ; PRIOR FILING DATE: 2000-10-12  
 ; NUMBER OF SEQ ID NOS: 1143  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 209  
 ; LENGTH: 1005  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: Incyte ID No. 6673549 221433.21  
 US-09-976-594-209

Query Match 26.7%; Score 16; DB 4; Length 1005;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CAGCGCCACCCGCACA 23  
 |||||  
 Db 22 CAGCGCCACCCGCACA 37

RESULT 5  
 US-09-252-991A-9440/c  
 ; Sequence 9440, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 107196.136  
 ; CURRENT APPLICATION NUMBER: US/09/252,991A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO 9440  
 ; LENGTH: 1371  
 ; TYPE: DNA  
 ; ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-9440

Query Match 26.7%; Score 16; DB 4; Length 1371;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 CGAGCGCTCCGGATAC 47  
 |||||  
 Db 164 CGAGCGCTCCGGATAC 149

RESULT 6

US-09-949-016-16571  
 ; Sequence 16571, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001307  
 ; CURRENT APPLICATION NUMBER: US/09/949,016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 16571  
 ; LENGTH: 36075  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 US-09-949-016-16571

Query Match 26.7%; Score 16; DB 4; Length 36075;  
 Best Local Similarity 100.0%; Pred. No. 9.8;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CACCCGCACATGGCGT 29  
 |||||  
 Db 25866 CACCCGCACATGGCGT 25881

RESULT 7

US-09-949-016-16572  
 ; Sequence 16572, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

```
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16572
; LENGTH: 36075
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16572

Query Match          26.7%; Score 16; DB 4; Length 36075;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 CACCGGCACATGGCGT 29
Db      25866 CACCGGCACATGGCGT 25881

RESULT 8
US-09-949-016-12788
; Sequence 12788, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12788
; LENGTH: 36625
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12788

Query Match          26.7%; Score 16; DB 4; Length 36625;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 CACCGGCACATGGCGT 29
Db      25866 CACCGGCACATGGCGT 25881

RESULT 9
US-09-949-016-16569
; Sequence 16569, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
```

```
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16569
; LENGTH: 37133
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16569

Query Match          26.7%; Score 16; DB 4; Length 37133;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 CACCGGCACATGGCGT 29
Db      25866 CACCGGCACATGGCGT 25881

RESULT 10
US-09-949-016-16570
; Sequence 16570, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16570
; LENGTH: 37133
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16570

Query Match          26.7%; Score 16; DB 4; Length 37133;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14 CACCGGCACATGGCGT 29
Db      25866 CACCGGCACATGGCGT 25881

RESULT 11
US-09-060-756-171/c
; Sequence 171, Application US/09060756
; Patent No. 6183957
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/09/060,756
; CURRENT FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.0
```

```
; SEQ ID NO 171
; LENGTH: 318
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (various positions within the sequence)
; OTHER INFORMATION: applicants are uncertain of bases designated as "n"
US-09-060-756-171

Query Match      25.0%; Score 15; DB 3; Length 318;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CAGCGCCACCCGCAC 22
      |||||
Db      316 CAGCGCCACCCGCAC 302

RESULT 12
US-09-670-314-171/c
; Sequence 171, Application US/09670314
; Patent No. 6492506
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/09/670,314
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/060,756
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 171
; LENGTH: 318
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (various positions within the sequence)
; OTHER INFORMATION: applicants are uncertain of bases designated as "n"
US-09-670-314-171

Query Match      25.0%; Score 15; DB 4; Length 318;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CAGCGCCACCCGCAC 22
      |||||
Db      316 CAGCGCCACCCGCAC 302

RESULT 13
US-09-060-756-397/c
; Sequence 397, Application US/09060756
; Patent No. 6183957
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/09/060,756
; CURRENT FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 397
; LENGTH: 350
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (various positions within the sequence)
; OTHER INFORMATION: applicants are uncertain of bases designated as "n"
US-09-670-314-397

Query Match      25.0%; Score 15; DB 4; Length 350;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CAGCGCCACCCGCAC 22
      |||||
Db      349 CAGCGCCACCCGCAC 335

RESULT 14
US-09-670-314-397/c
; Sequence 397, Application US/09670314
; Patent No. 6492506
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/09/670,314
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: 09/060,756
; PRIOR FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 397
; LENGTH: 350
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (various positions within the sequence)
; OTHER INFORMATION: applicants are uncertain of bases designated as "n"
US-09-670-314-397

Query Match      25.0%; Score 15; DB 4; Length 350;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 CAGCGCCACCCGCAC 22
      |||||
Db      349 CAGCGCCACCCGCAC 335

RESULT 15
US-09-060-756-137/c
; Sequence 137, Application US/09060756
; Patent No. 6183957
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/09/060,756
; CURRENT FILING DATE: 1998-04-16
```



; NUMBER OF SEQ ID NOS: 743  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 137  
; LENGTH: 357  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
US-09-060-756-137

Query Match 25.0%; Score 15; DB 3; Length 357;  
Best Local Similarity 100.0%; Pred. No. 53;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CAGCGCCACCCGCAC 22  
| | | | | | | | | |  
Db 353 CAGCGCCACCCGCAC 339

Search completed: June 30, 2005, 04:10:29  
Job time : 118.2 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 29, 2005, 23:23:45 ; Search time 230.7 Seconds  
(without alignments)  
1625.622 Million cell updates/sec

Title: US-10-057-136-12  
Perfect score: 60  
Sequence: 1 ggtagtagcgccaccgcg.....cggatacgagacggcgccct 60  
Scoring table: OLIGO-NUC  
Gapop-60.0, Gapext 60.0

Searched: 6067389 seqs, 3125258755 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 12134778

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:  
9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:  
13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:  
14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:  
15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:  
16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:  
17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:  
18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:  
19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq:  
20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq:  
21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq:  
22: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:  
23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq:  
24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:  
25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:  
26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	60	100.0	60	14	US-10-057-136-12
2	60	100.0	2297	17	US-10-406-317-41
3	17	28.3	479	20	US-10-425-115-81989
4	17	28.3	1593	15	US-10-156-761-7089
5	17	28.3	2175	17	US-10-282-122A-23932
6	17	28.3	9025608	15	US-10-156-761-1
7	16	26.7	464	18	US-10-424-599-80160

c	8	16	26.7	565	19	US-10-437-963-60711	Sequence 60711, A
	9	16	26.7	592	18	US-10-240-425-1352	Sequence 1352, Ap
c	10	16	26.7	1254	17	US-10-369-493-41496	Sequence 41496, A
c	11	16	26.7	1560	15	US-10-156-761-3612	Sequence 3612, Ap
c	12	16	26.7	1804	20	US-10-723-860-8253	Sequence 8253, Ap
c	13	16	26.7	2342	17	US-10-282-122A-31789	Sequence 31789, A
	14	16	26.7	3708	17	US-10-282-122A-24775	Sequence 24775, A
c	15	16	26.7	32204	9	US-09-764-855-327	Sequence 327, App
c	16	16	26.7	32204	10	US-09-764-872-517	Sequence 517, App
	17	16	26.7	32204	14	US-10-734-329-327	Sequence 327, App
	18	16	26.7	9025608	15	US-10-156-761-1	Sequence 1, Appli
c	19	15	25.0	318	16	US-10-259-678-171	Sequence 171, App
c	20	15	25.0	350	16	US-10-259-678-397	Sequence 397, App
c	21	15	25.0	357	16	US-10-259-678-137	Sequence 137, App
c	22	15	25.0	384	11	US-09-864-408A-8011	Sequence 8011, Ap
c	23	15	25.0	424	20	US-10-425-115-168534	Sequence 168534,
c	24	15	25.0	448	16	US-10-259-678-64	Sequence 64, Appl
c	25	15	25.0	472	20	US-10-425-115-20315	Sequence 20315, A
c	26	15	25.0	510	19	US-10-767-701-26375	Sequence 26375, A
	27	15	25.0	534	15	US-10-198-677-141	Sequence 141, App
	28	15	25.0	537	15	US-10-198-677-143	Sequence 143, App
	29	15	25.0	633	15	US-10-156-761-1896	Sequence 1896, Ap
	30	15	25.0	695	18	US-10-424-599-81094	Sequence 81094, A
	31	15	25.0	755	20	US-10-653-047-1635	Sequence 1635, Ap
	32	15	25.0	798	20	US-10-425-115-168658	Sequence 168658,
c	33	15	25.0	896	18	US-10-425-114-28350	Sequence 28350, A
	34	15	25.0	999	11	US-09-886-349A-40	Sequence 40, Appl
	35	15	25.0	999	15	US-10-193-002-52	Sequence 52, Appl
	36	15	25.0	999	15	US-10-084-843-52	Sequence 52, Appl
	37	15	25.0	999	16	US-10-098-732A-40	Sequence 40, Appl
c	38	15	25.0	1008	15	US-10-156-761-3554	Sequence 3554, Ap
c	39	15	25.0	1080	18	US-10-425-114-25072	Sequence 25072, A
c	40	15	25.0	1086	17	US-10-282-122A-26278	Sequence 26278, A
c	41	15	25.0	1089	17	US-10-282-122A-28323	Sequence 28323, A
	42	15	25.0	1122	17	US-10-369-493-44243	Sequence 44243, A
	43	15	25.0	1125	18	US-10-425-114-34515	Sequence 34515, A
	44	15	25.0	1125	20	US-10-425-115-65655	Sequence 65655, A
	45	15	25.0	1160	20	US-10-425-115-65685	Sequence 65685, A

ALIGNMENTS

RESULT 1  
US-10-057-136-12  
; Sequence 12, Application US/10057136  
; Publication No. US20030021770A1  
; GENERAL INFORMATION:  
; APPLICANT: SCHLOM, JEFFREY  
; APPLICANT: KANTOR, JUDITH  
; APPLICANT: KUFU, DONALD  
; APPLICANT: PANICALI, DENNIS  
; APPLICANT: GRITZ, LINDA  
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1  
; TITLE OF INVENTION: TUMOR-ASSOCIATED ANTIGEN  
; FILE REFERENCE: 700953/47113C  
; CURRENT APPLICATION NUMBER: US/10/057,136  
; CURRENT FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: 09/366,670  
; PRIOR FILING DATE: 1999-08-03  
; PRIOR APPLICATION NUMBER: PCT/US98/03693  
; PRIOR FILING DATE: 1998-02-24  
; PRIOR APPLICATION NUMBER: 60/038,253  
; PRIOR FILING DATE: 1997-02-24  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-057-136-12

Query Match 100.0%; Score 60; DB 14; Length 60;

Best Local Similarity 100.0%; Pred. No. 1e-24;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GGTAGTACAGCGCCACCGCACATGGCGTACGAGCGCTCCGGATACGAGACCGGCGCCT 60  
Db 1 GGTAGTACAGCGCCACCGCACATGGCGTACGAGCGCTCCGGATACGAGACCGGCGCCT 60

RESULT 2  
US-10-406-317-41  
; Sequence 41, Application US/10406317  
; Publication No. US20040019195A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlom, Jeffrey;  
; APPLICANT: Hodge, James;  
; APPLICANT: Panicali, Dennis  
; TITLE OF INVENTION: A recombinant vector expressing multiple constitutulatory  
; TITLE OF INVENTION: molecules and uses thereof  
; FILE REFERENCE: 38163-0189  
; CURRENT APPLICATION NUMBER: US/10/406,317  
; CURRENT FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: US/09/856,988  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: PCT/US99/26866  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/111,582  
; PRIOR FILING DATE: 1998-12-09  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 41  
; LENGTH: 2297  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: VECTOR  
US-10-406-317-41

Query Match 100.0%; Score 60; DB 17; Length 2297;  
Best Local Similarity 100.0%; Pred. No. 5.8e-25;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTAGTACAGCGCCACCGCACATGGCGTACGAGCGCTCCGGATACGAGACCGGCGCCT 60  
Db 886 GGTAGTACAGCGCCACCGCACATGGCGTACGAGCGCTCCGGATACGAGACCGGCGCCT 945

RESULT 3  
US-10-425-115-81989/c  
; Sequence 81989, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 81989  
; LENGTH: 479  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_174788C.1  
US-10-425-115-81989

Query Match 28.3%; Score 17; DB 20; Length 479;  
Best Local Similarity 100.0%; Pred. No. 5.5;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 CGCACATGGCGTCACGA 34  
Db 320 CGCACATGGCGTCACGA 304  
  
RESULT 4  
US-10-156-761-7089/c  
; Sequence 7089, Application US/10156761  
; Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADAYOSHI  
; APPLICANT: SAKAKI, YOSHIYUKI  
; APPLICANT: HATTORI, MASAHIRA  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-262  
; CURRENT APPLICATION NUMBER: US/10/156,761  
; CURRENT FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: JP 2001-204089  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 15109  
; SEQ ID NO 7089  
; LENGTH: 1593  
; TYPE: DNA  
; ORGANISM: Streptomyces avermitilis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1593)  
US-10-156-761-7089

Query Match 28.3%; Score 17; DB 15; Length 1593;  
Best Local Similarity 100.0%; Pred. No. 4.6;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 CGTCACGAGCGCTCCGG 43  
Db 63 CGTCACGAGCGCTCCGG 47

RESULT 5  
US-10-282-122A-23932  
; Sequence 23932, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.  
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A  
; CURRENT FILING DATE: 2003-02-20  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/230,335

```
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23932
; LENGTH: 2175
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-10-282-122A-23932

Query Match      28.3%; Score 17; DB 17; Length 2175;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 AGTACAGCGCCACCCGC 20
      |||||
Db      2021 AGTACAGCGCCACCCGC 2037

RESULT 6
US-10-156-761-1/c
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match      28.3%; Score 17; DB 15; Length 9025608;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      27 CGTCACGAGCGCTCCGG 43
      |||||
Db      8469210 CGTCACGAGCGCTCCGG 8469194

RESULT 7
US-10-424-599-80160/c
```

```
; Sequence 80160, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 80160
; LENGTH: 464
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_433C.1
US-10-424-599-80160
```

```
Query Match      26.7%; Score 16; DB 18; Length 464;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      42 GGATACGAGACCGCG 57
      |||||
Db      405 GGATACGAGACCGCG 390
```

```
RESULT 8
US-10-437-963-60711/c
; Sequence 60711, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 60711
; LENGTH: 565
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(565)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_62213C.1
US-10-437-963-60711
```

```
Query Match      26.7%; Score 16; DB 19; Length 565;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 CCCGCACATGGCGTCA 31
      |||||
Db      191 CCCGCACATGGCGTCA 176
```

```
RESULT 9
US-10-240-425-1352
; Sequence 1352, Application US/10240425
```

; Publication No. US20040033502A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Amanda  
; APPLICANT: Boland, Joseph F.  
; APPLICANT: Lord, Reginald V.  
; APPLICANT: Alvarez, Chris  
; APPLICANT: Wetzel, Jon C.  
; APPLICANT: Scherf, Uwe  
; APPLICANT: Vockley, Joseph G.  
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue  
; FILE REFERENCE: 44921-5026  
; CURRENT APPLICATION NUMBER: US/10/240,425  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: PCT/US01/09847  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: US 60/193,446  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 1588  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1352  
; LENGTH: 592  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. US20040033502A1 N30008  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(592)  
; OTHER INFORMATION: n = a o r c o r g o r t  
; US-10-240-425-1352

Query Match 26.7%; Score 16; DB 18; Length 592;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CAGCGCCACCCGCACA 23  
|||||  
Db 20 CAGCGCCACCCGCACA 35

RESULT 10  
US-10-369-493-41496/c  
; Sequence 41496, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 41496  
; LENGTH: 1254  
; TYPE: DNA  
; ORGANISM: SPHINGOMONAS  
; US-10-369-493-41496

Query Match 26.7%; Score 16; DB 17; Length 1254;  
Best Local Similarity 100.0%; Pred. No. 18;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GTACAGCGCCACCCGC 20  
|||||  
Db 954 GTACAGCGCCACCCGC 939

RESULT 11  
US-10-156-761-3612/c  
; Sequence 3612, Application US/10156761  
; Publication No. US20030119018A1  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADAYOSHI  
; APPLICANT: SAKAKI, YOSHIYUKI  
; APPLICANT: HATTORI, MASAHIRA  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-262  
; CURRENT APPLICATION NUMBER: US/10/156,761  
; CURRENT FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: JP 2001-204089  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 15109  
; SEQ ID NO 3612  
; LENGTH: 1560  
; TYPE: DNA  
; ORGANISM: Streptomyces avermitilis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1560)  
; US-10-156-761-3612

Query Match 26.7%; Score 16; DB 15; Length 1560;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CGCCACCCGCACATGG 26  
|||||  
Db 75 CGCCACCCGCACATGG 60

RESULT 12  
US-10-723-860-8253  
; Sequence 8253, Application US/10723860  
; Publication No. US20040253606A1  
; GENERAL INFORMATION:  
; APPLICANT: Aziz, Natasha  
; APPLICANT: Ginsburg, Wendy M.  
; APPLICANT: Zlotnik, Albert  
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &  
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators  
; FILE REFERENCE: 05882.0193.NPUS01  
; CURRENT APPLICATION NUMBER: US/10/723,860  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: 60/429,739  
; PRIOR FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 8393  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8253  
; LENGTH: 1804  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-10-723-860-8253

Query Match 26.7%; Score 16; DB 20; Length 1804;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CAGCGCCACCCGCACA 23  
|||||  
Db 307 CAGCGCCACCCGCACA 322

RESULT 13  
US-10-282-122A-31789/c

; Sequence 31789, Application US/10282122A  
; Publication No. US20040029129A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Liangsu  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Malone, Cheryl  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlsen, Kari  
; APPLICANT: Zyskind, Judith  
; APPLICANT: Wall, Daniel  
; APPLICANT: Trawick, John  
; APPLICANT: Carr, Grant  
; APPLICANT: Yamamoto, Robert  
; APPLICANT: Forsyth, R.  
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A  
; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 78614

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 31789

; LENGTH: 2342

; TYPE: DNA

; ORGANISM: Pseudomonas putida

US-10-282-122A-31789

Query Match 26.7%; Score 16; DB 17; Length 2342;

Best Local Similarity 100.0%; Pred. No. 16;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CACCCGCACATGGCGT 29

|||||

Db 1721 CACCCGCACATGGCGT 1706

RESULT 14

US-10-282-122A-24775

; Sequence 24775, Application US/10282122A

; Publication No. US20040029129A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu

; APPLICANT: Zamudio, Carlos

; APPLICANT: Malone, Cheryl

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari

; APPLICANT: Zyskind, Judith

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John

; APPLICANT: Carr, Grant

; APPLICANT: Yamamoto, Robert

; APPLICANT: Forsyth, R.

; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 78614

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 24775

; LENGTH: 3708

; TYPE: DNA

; ORGANISM: Listeria monocytogenes

US-10-282-122A-24775

Query Match 26.7%; Score 16; DB 17; Length 3708;

Best Local Similarity 100.0%; Pred. No. 15;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 ACGAGCGCTCCGGATA 46

|||||

Db 1789 ACGAGCGCTCCGGATA 1804

RESULT 15

US-09-764-855-327

; Sequence 327, Application US/09764855

; Patent No. US20020119919A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PA110

; CURRENT APPLICATION NUMBER: US/09/764,855

; CURRENT FILING DATE: 2001-01-17

; Prior application data removed - consult PALM or file wrapper

; NUMBER OF SEQ ID NOS: 334

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 327

; LENGTH: 32204

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-764-855-327

Query Match 26.7%; Score 16; DB 9; Length 32204;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CAGCGCCACCCGCACA 23

|||||

Db 76 CAGCGCCACCCGCACA 91

Search completed: June 30, 2005, 04:55:08

Job time : 370.7 secs





GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 29, 2005, 19:26:35 ; Search time 51.2 Seconds  
(without alignments)  
1917.512 Million cell updates/sec

Title: US-10-057-136-2  
Perfect score: 60  
Sequence: 1 ggctccaccgccccccagc.....cggacaccaggcgcccccg 60

Scoring table: ~~WILCOX~~  
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA: \*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq: \*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq: \*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq: \*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq: \*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq: \*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	100.0	1804	4	US-10-029-517-17 Sequence 17, Appl
2	60	100.0	8186	4	US-10-029-517-19 Sequence 19, Appl
3	57	95.0	518	4	US-10-029-517-101 Sequence 101, App
4	54	90.0	60	4	US-09-475-947A-246 Sequence 246, App
5	54	90.0	1721	4	US-10-029-517-3 Sequence 3, Appl
6	43	71.7	572	4	US-10-029-517-18 Sequence 18, Appl
7	27	45.0	6192	2	US-08-479-537A-1 Sequence 1, Appl
8	27	45.0	6192	3	US-09-083-116-1 Sequence 1, Appl
9	27	45.0	6192	3	US-09-134-916A-1 Sequence 1, Appl
10	27	45.0	6449	2	US-08-479-537A-4 Sequence 4, Appl
11	27	45.0	6449	3	US-09-083-116-4 Sequence 4, Appl
12	27	45.0	6449	3	US-09-134-916A-4 Sequence 4, Appl
13	23	38.3	981	4	US-10-029-517-16 Sequence 16, Appl
14	23	38.3	3343	4	US-10-029-517-102 Sequence 102, App
15	17	28.3	2001	4	US-09-489-039A-3650 Sequence 3650, App
16	17	28.3	2145	4	US-09-489-039A-3938 Sequence 3938, App
17	17	28.3	14516	4	US-09-949-016-17047 Sequence 17047, A
18	16	26.7	601	4	US-09-949-016-21132 Sequence 21132, A
19	16	26.7	601	4	US-09-949-016-21133 Sequence 21133, A
20	16	26.7	601	4	US-09-949-016-21134 Sequence 21134, A
21	16	26.7	601	4	US-09-949-016-36255 Sequence 36255, A
22	16	26.7	601	4	US-09-949-016-47500 Sequence 47500, A
23	16	26.7	601	4	US-09-949-016-47501 Sequence 47501, A
24	16	26.7	601	4	US-09-949-016-47502 Sequence 47502, A
25	16	26.7	601	4	US-09-949-016-51958 Sequence 51958, A
26	16	26.7	927	3	US-09-804-778A-1 Sequence 1, Appl
27	16	26.7	1431	4	US-09-252-991A-2821 Sequence 2821, Ap

c	28	16	26.7	1773	4	US-09-902-540-2394	Sequence 2394, Ap
c	29	16	26.7	2052	4	US-09-252-991A-3147	Sequence 3147, Ap
	30	16	26.7	8205	4	US-09-949-016-1500	Sequence 1500, Ap
	31	16	26.7	8220	4	US-09-949-016-932	Sequence 932, App
	32	16	26.7	15209	4	US-09-902-540-1104	Sequence 1104, Ap
c	33	16	26.7	31467	4	US-09-949-016-13134	Sequence 13134, A
c	34	16	26.7	31868	4	US-09-949-016-11907	Sequence 11907, A
c	35	16	26.7	101356	4	US-09-949-016-12364	Sequence 12364, A
c	36	16	26.7	101357	4	US-09-949-016-16924	Sequence 16924, A
c	37	16	26.7	151256	4	US-09-949-016-12674	Sequence 12674, A
	38	16	26.7	151261	4	US-09-949-016-13242	Sequence 13242, A
	39	16	26.7	186734	4	US-09-949-016-14870	Sequence 14870, A
	40	16	26.7	193689	4	US-09-949-016-12350	Sequence 12350, A
	41	16	26.7	193689	4	US-09-949-016-13088	Sequence 13088, A
c	42	16	26.7	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	43	16	26.7	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c	44	15	25.0	416	4	US-09-513-999C-8587	Sequence 8587, Ap
c	45	15	25.0	495	4	US-09-252-991A-6316	Sequence 6316, Ap

ALIGNMENTS

RESULT 1  
US-10-029-517-17  
; Sequence 17, Application US/10029517  
; Patent No. 6716627  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth W. Dobie  
; APPLICANT: Susan J. Myers  
; TITLE OF INVENTION: ANTISENSE MODULATION OF MUCIN 1, TRANSMEMBRANE EXPRESSION  
; FILE REFERENCE: RTS-0352  
; CURRENT APPLICATION NUMBER: US/10/029,517  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 107  
; SEQ ID NO 17  
; LENGTH: 1804  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (73) ... (1500)  
US-10-029-517-17

Query Match 100.0%; Score 60; DB 4; Length 1804;  
Best Local Similarity 100.0%; Pred. No. 1e-20;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGCTCCACCGCCCCCGCCAGCCCGGTGTCTACCTCGGCCCGGACACACCGCGGCCCG 60  
|||||  
Db 457 GGCTCCACCGCCCCCGCCAGCCCGGTGTCTACCTCGGCCCGGACACACCGCGGCCCG 516  
RESULT 2  
US-10-029-517-19  
; Sequence 19, Application US/10029517  
; Patent No. 6716627  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth W. Dobie  
; APPLICANT: Susan J. Myers  
; TITLE OF INVENTION: ANTISENSE MODULATION OF MUCIN 1, TRANSMEMBRANE EXPRESSION  
; FILE REFERENCE: RTS-0352  
; CURRENT APPLICATION NUMBER: US/10/029,517  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 107  
; SEQ ID NO 19  
; LENGTH: 8186  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: 6899  
; OTHER INFORMATION: unknown

NAME/KEY: unsure  
LOCATION: 7155  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 7184  
OTHER INFORMATION: unknown  
NAME/KEY: unsure  
LOCATION: 7957  
OTHER INFORMATION: unknown  
NAME/KEY: intron  
LOCATION: (2997)...(3498)  
OTHER INFORMATION: intron 1  
NAME/KEY: intron:exon junction  
LOCATION: (3498)...(3499)  
OTHER INFORMATION: intron 1:exon 2  
NAME/KEY: exon  
LOCATION: (3508)...(3599)  
OTHER INFORMATION: exon 2d  
NAME/KEY: exon:intron junction  
LOCATION: (3982)...(3983)  
OTHER INFORMATION: exon 2a:intron 2a  
NAME/KEY: intron:exon junction  
LOCATION: (4205)...(4206)  
OTHER INFORMATION: intron 2c:exon 3c  
NAME/KEY: intron:exon junction  
LOCATION: (4259)...(4260)  
OTHER INFORMATION: intron 2d:exon 3d  
NAME/KEY: exon  
LOCATION: (4260)...(4328)  
OTHER INFORMATION: exon 3d  
NAME/KEY: intron:exon junction  
LOCATION: (4632)...(4633)  
OTHER INFORMATION: intron 3:exon 4  
NAME/KEY: exon  
LOCATION: (4914)...(5035)  
OTHER INFORMATION: exon 5  
NAME/KEY: intron  
LOCATION: (5266)...(6293)  
OTHER INFORMATION: intron 6  
US-10-029-517-19

Query Match 100.0%; Score 60; DB 4; Length 8186;  
Best Local Similarity 100.0%; Pred. No. 8.8e-21;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTCCACCGCCCCCAGCCCGGTGTACCTCGGCCCGGACACCCAGCGCCCGG 60  
|||||  
Db 3825 GGCTCCACCGCCCCCAGCCCGGTGTACCTCGGCCCGGACACCCAGCGCCCGG 3884

RESULT 3  
US-10-029-517-101  
; Sequence 101, Application US/10029517  
; Patent No. 6716627  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth W. Dobie  
; APPLICANT: Susan J. Myers  
; TITLE OF INVENTION: ANTISENSE MODULATION OF MUCIN 1, TRANSMEMBRANE EXPRESSION  
; FILE REFERENCE: RTS-0352  
; CURRENT APPLICATION NUMBER: US/10/029,517  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 107  
; SEQ ID NO 101  
; LENGTH: 518  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
US-10-029-517-101

Query Match 95.0%; Score 57; DB 4; Length 518;  
Best Local Similarity 100.0%; Pred. No. 3.4e-19;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTCCACCGCCCCCAGCCCGGTGTACCTCGGCCCGGACACCCAGCGCCCGG 57  
|||||  
Db 462 GGCTCCACCGCCCCCAGCCCGGTGTACCTCGGCCCGGACACCCAGCGCCCGG 518

RESULT 4  
US-09-475-947A-246  
; Sequence 246, Application US/09475947A  
; Patent No. 6472154  
; GENERAL INFORMATION:  
; APPLICANT: Garner, Harold R.  
; APPLICANT: Wren, Jonathan D.  
; APPLICANT: Minna, John D.  
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes  
; FILE REFERENCE: UTSD0667  
; CURRENT APPLICATION NUMBER: US/09/475,947A  
; CURRENT FILING DATE: 1999-12-31  
; NUMBER OF SEQ ID NOS: 346  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 246  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: human  
US-09-475-947A-246

Query Match 90.0%; Score 54; DB 4; Length 60;  
Best Local Similarity 100.0%; Pred. No. 1.3e-17;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTCCACCGCCCCCAGCCCGGTGTACCTCGGCCCGGACACCCAGCGCCCGG 54  
|||||  
Db 7 GGCTCCACCGCCCCCAGCCCGGTGTACCTCGGCCCGGACACCCAGCGCCCGG 60

RESULT 5  
US-10-029-517-3  
; Sequence 3, Application US/10029517  
; Patent No. 6716627  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth W. Dobie  
; APPLICANT: Susan J. Myers  
; TITLE OF INVENTION: ANTISENSE MODULATION OF MUCIN 1, TRANSMEMBRANE EXPRESSION  
; FILE REFERENCE: RTS-0352  
; CURRENT APPLICATION NUMBER: US/10/029,517  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 107  
; SEQ ID NO 3  
; LENGTH: 1721  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (58)...(1605)  
US-10-029-517-3

Query Match 90.0%; Score 54; DB 4; Length 1721;  
Best Local Similarity 100.0%; Pred. No. 9.3e-18;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTCCACCGCCCCCAGCCCGGTGTACCTCGGCCCGGACACCCAGCGCCCGG 54  
|||||  
Db 442 GGCTCCACCGCCCCCAGCCCGGTGTACCTCGGCCCGGACACCCAGCGCCCGG 495

RESULT 6  
US-10-029-517-18  
; Sequence 18, Application US/10029517  
; Patent No. 6716627  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth W. Dobie  
; APPLICANT: Susan J. Myers  
; TITLE OF INVENTION: ANTISENSE MODULATION OF MUCIN 1, TRANSMEMBRANE EXPRESSION  
; FILE REFERENCE: RTS-0352

;; CURRENT APPLICATION NUMBER: US/10/029,517  
;; CURRENT FILING DATE: 2001-12-20  
;; NUMBER OF SEQ ID NOS: 107  
;; SEQ ID NO 18  
;; LENGTH: 572  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: (67)...(572)  
US-10-029-517-18

Query Match 71.7%; Score 43; DB 4; Length 572;  
Best Local Similarity 100.0%; Pred. No. 2.8e-12;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 AGCCACGGTGTACCTCGGCCCGGACACACGCGGCCCG 60  
|||||  
Db 495 AGCCACGGTGTACCTCGGCCCGGACACACGCGGCCCG 537  
|||||

RESULT 7  
US-08-479-537A-1  
; Sequence 1, Application US/08479537A  
; Patent No. 5861381  
; GENERAL INFORMATION:  
; APPLICANT: CHAMBON, Pierre  
; APPLICANT: KIENY, Marie-Paule  
; APPLICANT: LATHE, Richard  
; APPLICANT: HAREUVENI, Mara  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE  
; TITLE OF INVENTION: TREATMENT OR PREVENTION OF A MALIGNANT TUMOR  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/479,537A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: FR 90/13101  
; FILING DATE: 23-OCT-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/FR91/00835  
; FILING DATE: 23-OCT-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/039,320  
; FILING DATE: 04-APR-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/403,576  
; FILING DATE: 14-MAR-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 017753-025  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 836-6620  
; TELEFAX: (703) 836-2021  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6192 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single

;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; FEATURE:  
;; NAME/KEY: sig\_peptide  
;; LOCATION: 58..120  
;; FEATURE:  
;; NAME/KEY: repeat\_region  
;; LOCATION: 439..5239  
;; OTHER INFORMATION: /note= "The nucleotides spanning  
;; OTHER INFORMATION: 439-5239 constitute a repeated region wherein the repeat is 6  
;; OTHER INFORMATION: nucleotides and encodes 20 amino acids, 17 of which are fixed  
;; OTHER INFORMATION: The number of such repeats varies from 1 to 80."  
;; FEATURE:  
;; NAME/KEY: mat\_peptide  
;; LOCATION: 121..6166  
;; FEATURE:  
;; NAME/KEY: repeat\_region  
;; LOCATION: 457  
;; OTHER INFORMATION: /note= "Nucleotide 457 is X1 = NNN  
;; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA  
;; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."  
;; FEATURE:  
;; NAME/KEY: repeat\_region  
;; LOCATION: 487  
;; OTHER INFORMATION: /note= "Nucleotide 487 is Y = NNN  
;; OTHER INFORMATION: which is the codon for Thr or Asn wherein Thr = ACT, ACC, ACA  
;; OTHER INFORMATION: or ACG; and Asn = AAT or AAC."  
;; FEATURE:  
;; NAME/KEY: repeat\_region  
;; LOCATION: 496  
;; OTHER INFORMATION: /note= "Nucleotide 496 is X2 = NNN  
;; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA  
;; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."  
US-08-479-537A-1

Query Match 45.0%; Score 27; DB 2; Length 6192;  
Best Local Similarity 100.0%; Pred. No. 0.00018;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GCCCAGGTGTACCTCGGCCCGGAC 45  
|||||  
Db 460 GCCCAGGTGTACCTCGGCCCGGAC 486  
|||||

RESULT 8  
US-09-083-116-1  
; Sequence 1, Application US/09083116  
; Patent No. 6203795  
; GENERAL INFORMATION:  
; APPLICANT: CHAMBON, Pierre  
; APPLICANT: KIENY, Marie-Paule  
; APPLICANT: LATHE, Richard  
; APPLICANT: HAREUVENI, Mara  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE  
; TITLE OF INVENTION: TREATMENT OR PREVENTION OF A MALIGNANT TUMOR  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.  
; STREET: P.O. Box 1404  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: United States  
; ZIP: 22313-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/083,116  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:

```
; APPLICATION NUMBER: 08/479,537
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR91/00835
; FILING DATE: 23-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,320
; FILING DATE: 04-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,576
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 017753-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6192 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 58..120
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 439..5239
; OTHER INFORMATION: /note= "The nucleotides spanning
; OTHER INFORMATION: 439-5239 constitute a repeated region wherein the repeat is 6
; OTHER INFORMATION: nucleotides and encodes 20 amino acids, 17 of which are fixed
; OTHER INFORMATION: The number of such repeats varies from 1 to 80."
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 121..6166
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 457
; OTHER INFORMATION: /note= "Nucleotide 457 is X1 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 487
; OTHER INFORMATION: /note= "Nucleotide 487 is Y = NNN
; OTHER INFORMATION: which is the codon for Thr or Asn wherein Thr = ACT, ACC, ACA
; OTHER INFORMATION: or ACG; and Asn = AAT or AAC."
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 496
; OTHER INFORMATION: /note= "Nucleotide 496 is X2 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
;
; US-09-083-116-1
;
; Query Match 45.0%; Score 27; DB 3; Length 6192;
; Best Local Similarity 100.0%; Pred. No. 0.00018;
; Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 19 GCCACGGTGTACCTCGGCCCGGAC 45
; |||||
; Db 460 GCCACGGTGTACCTCGGCCCGGAC 486
;
; RESULT 9
; US-09-134-916A-1
; Sequence 1, Application US/09134916A
; Patent No. 6328956
; GENERAL INFORMATION:
; APPLICANT: CHAMBON, Pierre
```

```
; APPLICANT: KIENY, Marie-Paule
; APPLICANT: LATHE, Richard
; APPLICANT: HAREUVENI, Mara
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE
; TITLE OF INVENTION: TREATMENT OR PREVENTION OF A MALIGNANT TUMOR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,916A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,537
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: FR 90/13101
; FILING DATE: 23-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR91/00835
; FILING DATE: 23-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,320
; FILING DATE: 04-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,576
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 017753-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6192 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 58..120
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 439..5239
; OTHER INFORMATION: /note= "The nucleotides spanning
; OTHER INFORMATION: 439-5239 constitute a repeated region wherein the repeat is 6
; OTHER INFORMATION: nucleotides and encodes 20 amino acids, 17 of which are fixed
; OTHER INFORMATION: The number of such repeats varies from 1 to 80."
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 121..6166
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 457
; OTHER INFORMATION: /note= "Nucleotide 457 is X1 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 487
; OTHER INFORMATION: /note= "Nucleotide 487 is Y = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
;
; US-09-134-916A-1
; Sequence 1, Application US/09134916A
; Patent No. 6328956
; GENERAL INFORMATION:
; APPLICANT: CHAMBON, Pierre
```

```

; OTHER INFORMATION: which is the codon for Thr or Asn wherein Thr = ACT, ACC, ACA
; OTHER INFORMATION: or ACG; and Asn = AAT or AAC."
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 496
; OTHER INFORMATION: /note= "Nucleotide 496 is X2 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
US-09-134-916A-1

Query Match 45.0%; Score 27; DB 3; Length 6192;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GCCCAGGTGTCTACCTCGGCCCGGAC 45
   |||||
Db 460 GCCCAGGTGTCTACCTCGGCCCGGAC 486

RESULT 10
US-08-479-537A-4
; Sequence 4, Application US/08479537A
; Patent No. 5861381
; GENERAL INFORMATION:
; APPLICANT: CHAMBER, Pierre
; APPLICANT: KIENY, Marie-Paule
; APPLICANT: LATHE, Richard
; APPLICANT: HAREUVENI, Mara
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE
; TITLE OF INVENTION: TREATMENT OR PREVENTION OF A MALIGNANT TUMOR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,537A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 90/13101
; FILING DATE: 23-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR91/00835
; FILING DATE: 23-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,320
; FILING DATE: 04-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,576
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 017753-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6449 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

```

```

; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 58..120
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 439..5239
; OTHER INFORMATION: /note= "The nucleotides spanning
; OTHER INFORMATION: 439-5239 constitute a repeated region wherein the repeat is 6
; OTHER INFORMATION: nucleotides and encodes 20 amino acids, 17 of which are fixed
; OTHER INFORMATION: The number of such repeats varies from 1 to 80."
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 121..5661
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 457
; OTHER INFORMATION: /note= "Nucleotide 457 is X1 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 487
; OTHER INFORMATION: /note= "Nucleotide 487 is Y = NNN
; OTHER INFORMATION: which is the codon for Thr or Asn wherein Thr = ACT, ACC, ACA
; OTHER INFORMATION: or ACG; and Asn = AAT or AAC."
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 496
; OTHER INFORMATION: /note= "Nucleotide 496 is X2 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
US-08-479-537A-4

Query Match 45.0%; Score 27; DB 2; Length 6449;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GCCCAGGTGTCTACCTCGGCCCGGAC 45
   |||||
Db 460 GCCCAGGTGTCTACCTCGGCCCGGAC 486

RESULT 11
US-09-083-116-4
; Sequence 4, Application US/09083116
; Patent No. 6203795
; GENERAL INFORMATION:
; APPLICANT: CHAMBER, Pierre
; APPLICANT: KIENY, Marie-Paule
; APPLICANT: LATHE, Richard
; APPLICANT: HAREUVENI, Mara
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE
; TITLE OF INVENTION: TREATMENT OR PREVENTION OF A MALIGNANT TUMOR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/083,116
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/479,537
; FILING DATE:

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR91/00835
; FILING DATE: 23-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,320
; FILING DATE: 04-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,576
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 017753-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6449 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 58..120
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 439..5239
; OTHER INFORMATION: /note= "The nucleotides spanning
; OTHER INFORMATION: 439-5239 constitute a repeated region wherein the repeat is 6
; OTHER INFORMATION: nucleotides and encodes 20 amino acids, 17 of which are fixed
; OTHER INFORMATION: The number of such repeats varies from 1 to 80."
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 121..5661
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 457
; OTHER INFORMATION: /note= "Nucleotide 457 is X1 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 487
; OTHER INFORMATION: /note= "Nucleotide 487 is Y = NNN
; OTHER INFORMATION: which is the codon for Thr or Asn wherein Thr = ACT, ACC, ACA
; OTHER INFORMATION: or ACG; and Asn = AAT or AAC."
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 496
; OTHER INFORMATION: /note= "Nucleotide 496 is X2 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
;
US-09-083-116-4
Query Match 45.0%; Score 27; DB 3; Length 6449;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 GCCCAGGTGTACCTCGGCCCGGAC 45
| | | | | | | | | | | | | | | | | | | | |
Db 460 GCCCAGGTGTACCTCGGCCCGGAC 486

RESULT 12
US-09-134-916A-4
; Sequence 4, Application US/09134916A
; Patent No. 6328956
; GENERAL INFORMATION:
; APPLICANT: CHAMBON, Pierre
; APPLICANT: KIENY, Marie-Paule
; APPLICANT: LATHE, Richard

```

```

; APPLICANT: HAREUVENI, Mara
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE
; TITLE OF INVENTION: TREATMENT OR PREVENTION OF A MALIGNANT TUMOR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,916A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,537
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: FR 90/13101
; FILING DATE: 23-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR91/00835
; FILING DATE: 23-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,320
; FILING DATE: 04-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,576
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 017753-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6449 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 58..120
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 439..5239
; OTHER INFORMATION: /note= "The nucleotides spanning
; OTHER INFORMATION: 439-5239 constitute a repeated region wherein the repeat is 6
; OTHER INFORMATION: nucleotides and encodes 20 amino acids, 17 of which are fixed
; OTHER INFORMATION: The number of such repeats varies from 1 to 80."
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 121..5661
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 457
; OTHER INFORMATION: /note= "Nucleotide 457 is X1 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 487
; OTHER INFORMATION: /note= "Nucleotide 487 is Y = NNN
; OTHER INFORMATION: which is the codon for Thr or Asn wherein Thr = ACT, ACC, ACA
; OTHER INFORMATION: or ACG; and Asn = AAT or AAC."

```



```

; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 496
; OTHER INFORMATION: /note= "Nucleotide 496 is X2 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
US-09-134-916A-4

```

```

Query Match 45.0%; Score 27; DB 3; Length 6449;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 19 GCCACGGTGTACCTCGGCCCGGAC 45
|||||
Db 460 GCCACGGTGTACCTCGGCCCGGAC 486

```

```

RESULT 13
US-10-029-517-16
; Sequence 16, Application US/10029517
; Patent No. 6716627
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Susan J. Myers
; TITLE OF INVENTION: ANTISENSE MODULATION OF MUCIN 1, TRANSMEMBRANE EXPRESSION
; FILE REFERENCE: RTS-0352
; CURRENT APPLICATION NUMBER: US/10/029,517
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 107
; SEQ ID NO 16
; LENGTH: 981
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon:exon junction
; LOCATION: (464)...(465)
; OTHER INFORMATION: exon 3b:exon 4
US-10-029-517-16

```

```

Query Match 38.3%; Score 23; DB 4; Length 981;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GGCTCCACCGCCCCCGGCCCA 23
|||||
Db 21 GGCTCCACCGCCCCCGGCCCA 43

```

```

RESULT 14
US-10-029-517-102
; Sequence 102, Application US/10029517
; Patent No. 6716627
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Susan J. Myers
; TITLE OF INVENTION: ANTISENSE MODULATION OF MUCIN 1, TRANSMEMBRANE EXPRESSION
; FILE REFERENCE: RTS-0352
; CURRENT APPLICATION NUMBER: US/10/029,517
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 107
; SEQ ID NO 102
; LENGTH: 3343
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-10-029-517-102

```

```

Query Match 38.3%; Score 23; DB 4; Length 3343;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GGCTCCACCGCCCCCGGCCCA 23
|||||

```

```

Db 1668 GGCTCCACCGCCCCCGGCCCA 1690

```

```

RESULT 15
US-09-489-039A-3650/c
; Sequence 3650, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709,2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 3650
; LENGTH: 2001
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-3650

```

```

Query Match 28.3%; Score 17; DB 4; Length 2001;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 37 GCCCCGGACACCCAGGCC 53
|||||
Db 920 GCCCCGGACACCCAGGCC 904

```

```

Search completed: June 30, 2005, 04:01:15
Job time : 178.2 secs

```

**THIS PAGE BLANK (USPTO)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 29, 2005, 23:23:45 ; Search time 230.7 Seconds  
(without alignments)  
1625.622 Million cell updates/sec

Title: US-10-057-136-2  
Perfect score: 60  
Sequence: 1 ggtccacgccccccagc.....cggacaccagggcccg 60

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 6067389 seqs, 3125258755 residues

Word size : 0

Total number of hits satisfying chosen parameters: 12134778

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:  
9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:  
13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:  
14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:  
15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:  
16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:  
17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:  
18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:  
19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq:  
20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq:  
21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq:  
22: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:  
23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq:  
24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:  
25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:  
26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	100.0	60	14	US-10-057-136-2
2	60	100.0	1424	17	US-10-447-839A-75
3	60	100.0	1424	21	US-10-778-859-75
4	60	100.0	1428	17	US-10-447-839A-20
5	60	100.0	1428	21	US-10-778-859-20
6	60	100.0	1527	14	US-10-057-136-19
7	60	100.0	1799	17	US-10-447-839A-19

Query Match 100.0%; Score 60; DB 14; Length 60;

ALIGNMENTS

RESULT 1  
US-10-057-136-2  
; Sequence 2, Application US/10057136  
; Publication No. US20030021770A1  
; GENERAL INFORMATION:  
; APPLICANT: SCHLOM, JEFFREY  
; APPLICANT: KANTOR, JUDITH  
; APPLICANT: KUFU, DONALD  
; APPLICANT: PANICALI, DENNIS  
; APPLICANT: GRITZ, LINDA  
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1  
; TITLE OF INVENTION: TUMOR-ASSOCIATED ANTIGEN  
; FILE REFERENCE: 700953/47113C  
; CURRENT APPLICATION NUMBER: US/10/057,136  
; CURRENT FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: 09/366,670  
; PRIOR FILING DATE: 1999-08-03  
; PRIOR APPLICATION NUMBER: PCT/US98/03693  
; PRIOR FILING DATE: 1998-02-24  
; PRIOR APPLICATION NUMBER: 60/038,253  
; PRIOR FILING DATE: 1997-02-24  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-057-136-2

8	60	100.0	1799	21	US-10-778-859-19	Sequence 19, Appl
9	60	100.0	1804	9	US-09-964-824A-573	Sequence 573, App
10	60	100.0	1804	15	US-10-029-517-17	Sequence 17, Appl
11	60	100.0	1804	19	US-10-717-597-30	Sequence 30, Appl
12	60	100.0	1804	19	US-10-775-920-84	Sequence 84, Appl
13	60	100.0	1804	21	US-10-843-641A-5876	Sequence 5876, Ap
14	60	100.0	1823	15	US-10-101-510-339	Sequence 339, App
15	60	100.0	2297	17	US-10-406-317-41	Sequence 41, Appl
16	60	100.0	4139	9	US-09-964-824A-105	Sequence 105, App
17	60	100.0	4139	9	US-09-964-824A-578	Sequence 578, App
18	60	100.0	4139	9	US-09-864-864-334	Sequence 334, App
19	60	100.0	4139	9	US-09-880-107-2121	Sequence 2121, Ap
20	60	100.0	4139	11	US-09-968-007A-751	Sequence 751, App
21	60	100.0	4139	14	US-10-171-311-157	Sequence 157, App
22	60	100.0	4139	15	US-10-177-293-310	Sequence 310, App
23	60	100.0	4139	17	US-10-440-464-155	Sequence 155, App
24	60	100.0	4139	19	US-10-734-564-53	Sequence 53, Appl
25	60	100.0	4139	19	US-10-775-920-80	Sequence 80, Appl
26	60	100.0	4139	19	US-10-775-920-85	Sequence 85, Appl
27	60	100.0	4139	21	US-10-843-641A-5408	Sequence 5408, Ap
28	60	100.0	4139	21	US-10-843-641A-5881	Sequence 5881, Ap
29	60	100.0	4139	21	US-10-843-641A-7221	Sequence 7221, Ap
30	60	100.0	8181	11	US-09-951-938-18	Sequence 18, Appl
31	60	100.0	8181	17	US-10-447-839A-18	Sequence 18, Appl
32	60	100.0	8181	21	US-10-778-859-18	Sequence 18, Appl
33	60	100.0	8186	15	US-10-029-517-19	Sequence 19, Appl
34	60	100.0	8186	21	US-10-696-639-21	Sequence 21, Appl
35	57	95.0	518	15	US-10-029-517-101	Sequence 101, App
36	54	90.0	1721	9	US-09-864-864-280	Sequence 280, App
37	54	90.0	1721	9	US-09-967-768A-224	Sequence 224, App
38	54	90.0	1721	14	US-10-097-340-211	Sequence 211, App
39	54	90.0	1721	14	US-10-171-311-155	Sequence 155, App
40	54	90.0	1721	15	US-10-007-926A-58	Sequence 58, Appl
41	54	90.0	1721	15	US-10-029-517-3	Sequence 3, Appli
42	54	90.0	1721	17	US-10-172-118-775	Sequence 775, App
43	54	90.0	1721	18	US-10-342-887-775	Sequence 775, App
44	54	90.0	1721	19	US-10-775-920-88	Sequence 88, Appl
45	54	90.0	1721	21	US-10-843-641A-6369	Sequence 6369, Ap



Query Match 100.0%; Score 60; DB 21; Length 1428;  
Best Local Similarity 93.3%; Pred. No. 1.8e-22;  
Matches 56; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTCCACCGCCCCCAGCCACGGTGTACCTCGGCCCGGACACACAGCGGCCCG 60  
Db 385 GGUCCACCGCCCCCAGCCACGGUGUCACUCGCGCCCGGACACACAGCGGCCCG 444

RESULT 6  
US-10-057-136-19  
; Sequence 19, Application US/10057136  
; Publication No. US20030021770A1  
; GENERAL INFORMATION:  
; APPLICANT: SCHLOM, JEFFREY  
; APPLICANT: KANTOR, JUDITH  
; APPLICANT: KUFU, DONALD  
; APPLICANT: PANICALI, DENNIS  
; APPLICANT: GRITZ, LINDA  
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1  
; FILE REFERENCE: 700953/47113C  
; CURRENT APPLICATION NUMBER: US/10/057,136  
; CURRENT FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: 09/366,670  
; PRIOR FILING DATE: 1999-08-03  
; PRIOR APPLICATION NUMBER: PCT/US98/03693  
; PRIOR FILING DATE: 1998-02-24  
; PRIOR APPLICATION NUMBER: 60/038,253  
; PRIOR FILING DATE: 1997-02-24  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 19  
; LENGTH: 1527  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-057-136-19

Query Match 100.0%; Score 60; DB 14; Length 1527;  
Best Local Similarity 100.0%; Pred. No. 1.8e-22;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTCCACCGCCCCCAGCCACGGTGTACCTCGGCCCGGACACACAGCGGCCCG 60  
Db 226 GGCTCCACCGCCCCCAGCCACGGTGTACCTCGGCCCGGACACACAGCGGCCCG 285

RESULT 7  
US-10-447-839A-19  
; Sequence 19, Application US/10447839A  
; Publication No. US20040018181A1  
; GENERAL INFORMATION:  
; APPLICANT: Kufe, Donald W.  
; APPLICANT: Kharbanda, Surender  
; APPLICANT: Weitman, Steven D.  
; TITLE OF INVENTION: MUC1 INTERFERENCE RNA COMPOSITIONS AND METHODS DERIVED THEREFROM  
; FILE REFERENCE: 1000.05.009  
; CURRENT APPLICATION NUMBER: US/10/447,839A  
; CURRENT FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: 10/293,391  
; PRIOR FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: 09/951,938  
; PRIOR FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: 60/231,841  
; PRIOR FILING DATE: 2000-09-11  
; NUMBER OF SEQ ID NOS: 109  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 19  
; LENGTH: 1799  
; TYPE: RNA  
; ORGANISM: RNA  
US-10-447-839A-19

Query Match 100.0%; Score 60; DB 17; Length 1799;  
Best Local Similarity 93.3%; Pred. No. 1.7e-22;  
Matches 56; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTCCACCGCCCCCAGCCACGGTGTACCTCGGCCCGGACACACAGCGGCCCG 60  
Db 453 GGUCCACCGCCCCCAGCCACGGUGUCACUCGCGCCCGGACACACAGCGGCCCG 512

RESULT 8  
US-10-778-859-19  
; Sequence 19, Application US/10778859  
; Publication No. US20050042209A1  
; GENERAL INFORMATION:  
; APPLICANT: Kufe, Donald W.  
; APPLICANT: Ohno, Tsuneya.  
; TITLE OF INVENTION: MUC1 EXTRACELLULAR DOMAIN AND CANCER TREATMENT COMPOSITIONS AND  
; TITLE OF INVENTION: METHODS DERIVED THEREFROM  
; FILE REFERENCE: 1000.05.011  
; CURRENT APPLICATION NUMBER: US/10/778,859  
; CURRENT FILING DATE: 2004-02-13  
; PRIOR APPLICATION NUMBER: 10/293,391  
; PRIOR FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: 10/447,839  
; PRIOR FILING DATE: 2003-05-29  
; PRIOR APPLICATION NUMBER: 09/951,938  
; PRIOR FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: 60/231,841  
; PRIOR FILING DATE: 2000-09-11  
; NUMBER OF SEQ ID NOS: 111  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 19  
; LENGTH: 1799  
; TYPE: RNA  
; ORGANISM: RNA  
US-10-778-859-19

Query Match 100.0%; Score 60; DB 21; Length 1799;  
Best Local Similarity 93.3%; Pred. No. 1.7e-22;  
Matches 56; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCTCCACCGCCCCCAGCCACGGTGTACCTCGGCCCGGACACACAGCGGCCCG 60  
Db 453 GGUCCACCGCCCCCAGCCACGGUGUCACUCGCGCCCGGACACACAGCGGCCCG 512

RESULT 9  
US-09-964-824A-573  
; Sequence 573, Application US/09964824A  
; Patent No. US20020102531A1  
; GENERAL INFORMATION:  
; APPLICANT: Horrigan, Stephen  
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu  
; TITLE OF INVENTION: Sets  
; FILE REFERENCE: 689290-73  
; CURRENT APPLICATION NUMBER: US/09/964,824A  
; CURRENT FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: US/60/236,033  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US/60/236,032  
; PRIOR FILING DATE: 2000-09-28  
; PRIOR APPLICATION NUMBER: US/60/236,028  
; PRIOR FILING DATE: 2000-09-28  
; NUMBER OF SEQ ID NOS: 583  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 573  
; LENGTH: 1804  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-964-824A-573

Query Match 100.0%; Score 60; DB 9; Length 1804;

```
Best Local Similarity 100.0%; Pred. No. 1.7e-22;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTCCACCGCCCCCAGCCACGGTGTACCTCGGCCCGGACACACAGCGGCCCG 60
Db 457 GGCTCCACCGCCCCCAGCCACGGTGTACCTCGGCCCGGACACACAGCGGCCCG 516

RESULT 10
US-10-029-517-17
; Sequence 17, Application US/10029517
; Publication No. US20030148969A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Susan J. Myers
; TITLE OF INVENTION: ANTISENSE MODULATION OF MUCIN 1, TRANSMEMBRANE EXPRESSION
; FILE REFERENCE: RTS-0352
; CURRENT APPLICATION NUMBER: US/10/029,517
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 107
; SEQ ID NO 17
; LENGTH: 1804
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (73)...(1500)
US-10-029-517-17

Query Match 100.0%; Score 60; DB 15; Length 1804;
Best Local Similarity 100.0%; Pred. No. 1.7e-22;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTCCACCGCCCCCAGCCACGGTGTACCTCGGCCCGGACACACAGCGGCCCG 60
Db 457 GGCTCCACCGCCCCCAGCCACGGTGTACCTCGGCCCGGACACACAGCGGCCCG 516

RESULT 11
US-10-717-597-30
; Sequence 30, Application US/10717597
; Publication No. US20040110221A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael E.
; APPLICANT: Twine, Natalie C.
; APPLICANT: Dorner, Andrew J.
; APPLICANT: Trepicchio, William L.
; APPLICANT: Slonim, Donna K.
; APPLICANT: Stover, Jennifer A.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS
; FILE REFERENCE: AM101080L
; CURRENT APPLICATION NUMBER: US/10/717,597
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/459,782
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/427,982
; PRIOR FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 4904
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 1804
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-717-597-30

Query Match 100.0%; Score 60; DB 19; Length 1804;
Best Local Similarity 100.0%; Pred. No. 1.7e-22;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTCCACCGCCCCCAGCCACGGTGTACCTCGGCCCGGACACACAGCGGCCCG 60
Db 457 GGCTCCACCGCCCCCAGCCACGGTGTACCTCGGCCCGGACACACAGCGGCCCG 516
```

```
RESULT 12
US-10-775-920-84
; Sequence 84, Application US/10775920
; Publication No. US20040175744A1
; GENERAL INFORMATION:
; APPLICANT: Mergen Ltd
; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCES AND CORRESPONDING ENCODED POLYPEPTIDES
; TITLE OF INVENTION: OF PARTICULAR SECRETED AND MEMBRANE-BOUND PROTEINS OVEREXPRESSED
; TITLE OF INVENTION: IN CERTAIN CANCERS
; FILE REFERENCE: Mergen - 0010B
; CURRENT APPLICATION NUMBER: US/10/775,920
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 60/447,900
; PRIOR FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 385
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 84
; LENGTH: 1804
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-920-84

Query Match 100.0%; Score 60; DB 19; Length 1804;
Best Local Similarity 100.0%; Pred. No. 1.7e-22;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTCCACCGCCCCCAGCCACGGTGTACCTCGGCCCGGACACACAGCGGCCCG 60
Db 457 GGCTCCACCGCCCCCAGCCACGGTGTACCTCGGCCCGGACACACAGCGGCCCG 516

RESULT 13
US-10-843-641A-5876
; Sequence 5876, Application US/10843641A
; Publication No. US20050064454A1
; GENERAL INFORMATION:
; APPLICANT: Avalon Pharmaceuticals, Inc.
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; TITLE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-189
; CURRENT APPLICATION NUMBER: US/10/843,641A
; CURRENT FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: US/09/873,367
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US/09/954,531
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/954,456
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,436
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/09/964,824
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/09/967,768
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US/09/968,007
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,347
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/09/969,708
; PRIOR FILING DATE: 2001-10-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 8447
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5876
; LENGTH: 1804
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-843-641A-5876
```

Query Match 100.0%; Score 60; DB 21; Length 1804;  
Best Local Similarity 100.0%; Pred. No. 1.7e-22;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGCTCCACCGCCCCCAGCCCGGTGTACCTCGGCCCGGACACAGGCGGCCCG 60  
|||||  
Db 457 GGCTCCACCGCCCCCAGCCCGGTGTACCTCGGCCCGGACACAGGCGGCCCG 516  
|||||

RESULT 14  
US-10-101-510-339  
; Sequence 339, Application US/10101510  
; Publication No. US20030148295A1  
; GENERAL INFORMATION:  
; APPLICANT: WAN, JACKSON  
; APPLICANT: WANG, YIXIN  
; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE  
; FILE REFERENCE: 15117.0012  
; CURRENT APPLICATION NUMBER: US/10/101,510  
; CURRENT FILING DATE: 2002-03-20  
; PRIOR APPLICATION NUMBER: 60/276,947  
; PRIOR FILING DATE: 2001-03-20  
; NUMBER OF SEQ ID NOS: 805  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 339  
; LENGTH: 1823  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-101-510-339

Query Match 100.0%; Score 60; DB 15; Length 1823;  
Best Local Similarity 100.0%; Pred. No. 1.7e-22;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGCTCCACCGCCCCCAGCCCGGTGTACCTCGGCCCGGACACAGGCGGCCCG 60  
|||||  
Db 457 GGCTCCACCGCCCCCAGCCCGGTGTACCTCGGCCCGGACACAGGCGGCCCG 516  
|||||

RESULT 15  
US-10-406-317-41  
; Sequence 41, Application US/10406317  
; Publication No. US20040019195A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlom, Jeffrey;  
; APPLICANT: Hodge, James;  
; APPLICANT: Panicali, Dennis  
; TITLE OF INVENTION: A recombinant vector expressing multiple constimulatory  
; TITLE OF INVENTION: molecules and uses thereof  
; FILE REFERENCE: 38163-0189  
; CURRENT APPLICATION NUMBER: US/10/406,317  
; CURRENT FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: US/09/856,988  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: PCT/US99/26866  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/111,582  
; PRIOR FILING DATE: 1998-12-09  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 41  
; LENGTH: 2297  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: VECTOR  
; OTHER INFORMATION: SEQUENCE  
US-10-406-317-41

Query Match 100.0%; Score 60; DB 17; Length 2297;  
Best Local Similarity 100.0%; Pred. No. 1.6e-22;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCTCCACCGCCCCCAGCCCGGTGTACCTCGGCCCGGACACAGGCGGCCCG 60  
|||||  
Db 346 GGCTCCACCGCCCCCAGCCCGGTGTACCTCGGCCCGGACACAGGCGGCCCG 405  
|||||

Search completed: June 30, 2005, 04:39:02  
Job time : 247.7 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 29, 2005, 19:26:35 ; Search time 51.2 Seconds  
(without alignments)  
1917.512 Million cell updates/sec

Title: US-10-057-136-5  
Perfect score: 60  
Sequence: 1 ggtaccacgcgcgcctgc.....ccgacacgcgcgcctccc 60

Scoring table:  Gapop 60.0, Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA:\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	30.0	284	1 US-08-150-203A-2	Sequence 2, Appli
2	18	30.0	284	1 US-08-454-730-2	Sequence 2, Appli
3	18	30.0	284	3 US-08-949-788-2	Sequence 2, Appli
4	18	30.0	1289	2 US-08-344-833-1	Sequence 1, Appli
5	18	30.0	4190	3 US-08-924-345-1	Sequence 1, Appli
6	17	28.3	1110	4 US-09-252-991A-8962	Sequence 8962, Ap
7	17	28.3	1278	4 US-09-252-991A-9043	Sequence 9043, Ap
8	17	28.3	1968	4 US-09-252-991A-8743	Sequence 8743, Ap
9	17	28.3	80161	3 US-09-036-987A-1	Sequence 1, Appli
10	17	28.3	80161	3 US-09-370-700-1	Sequence 1, Appli
11	17	28.3	80161	4 US-09-603-207-1	Sequence 1, Appli
12	16	26.7	25	4 US-09-396-196G-98221	Sequence 98221, A
13	16	26.7	25	4 US-09-396-196G-98222	Sequence 98222, A
14	16	26.7	327	4 US-09-902-540-4050	Sequence 4050, Ap
15	16	26.7	1122	4 US-09-252-991A-12729	Sequence 12729, A
16	16	26.7	1152	4 US-09-252-991A-12886	Sequence 12886, A
17	16	26.7	3772	4 US-09-962-665-5	Sequence 5, Appli
18	16	26.7	3772	4 US-09-963-333-5	Sequence 5, Appli
19	16	26.7	3772	4 US-09-962-677-5	Sequence 5, Appli
20	16	26.7	21511	4 US-09-902-540-1201	Sequence 1201, Ap
21	16	26.7	36241	4 US-08-311-731A-134	Sequence 134, App
22	16	26.7	68750	3 US-09-335-409-1	Sequence 1, Appli
23	16	26.7	68750	3 US-09-568-102-1	Sequence 1, Appli
24	16	26.7	68750	3 US-09-567-969-1	Sequence 1, Appli
25	16	26.7	68750	3 US-09-568-480-1	Sequence 1, Appli
26	16	26.7	68750	3 US-09-568-486-1	Sequence 1, Appli
27	16	26.7	68750	3 US-09-568-472-1	Sequence 1, Appli

c 28	16	26.7	68750	3	US-09-567-899-1	Sequence 1, Appli
c 29	16	26.7	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c 30	16	26.7	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c 31	15	25.0	288	4	US-09-313-294A-741	Sequence 741, App
c 32	15	25.0	292	4	US-09-313-294A-611	Sequence 611, App
c 33	15	25.0	414	4	US-09-252-991A-334	Sequence 334, App
c 34	15	25.0	432	4	US-09-621-976-9152	Sequence 9152, Ap
c 35	15	25.0	437	4	US-09-620-312D-1086	Sequence 1086, Ap
c 36	15	25.0	465	3	US-09-149-476-77	Sequence 77, Appl
c 37	15	25.0	468	4	US-09-252-991A-15459	Sequence 15459, A
c 38	15	25.0	480	4	US-09-252-991A-15417	Sequence 15417, A
c 39	15	25.0	771	4	US-09-252-991A-1476	Sequence 1476, Ap
c 40	15	25.0	825	4	US-09-902-540-3887	Sequence 3887, Ap
c 41	15	25.0	828	4	US-09-252-991A-1701	Sequence 1701, Ap
c 42	15	25.0	1014	4	US-09-252-991A-15280	Sequence 15280, A
c 43	15	25.0	1017	4	US-09-252-991A-15357	Sequence 15357, A
c 44	15	25.0	1071	4	US-09-902-540-5623	Sequence 5623, Ap
c 45	15	25.0	1086	4	US-09-902-540-5366	Sequence 5366, Ap

ALIGNMENTS

RESULT 1  
US-08-150-203A-2  
; Sequence 2, Application US/08150203A  
; Patent No. 5676951  
; GENERAL INFORMATION:  
; APPLICANT: Rijsewijk, Franciscus Antonius Maria  
; APPLICANT: van Oirschot, Johannes Theodorus  
; APPLICANT: Maes, Roger Kamel  
; TITLE OF INVENTION: Bovine Herpesvirus Type 1  
; TITLE OF INVENTION: Deletion Mutants, Vaccines Based  
; TITLE OF INVENTION: Thereon, Diagnostic Kits For  
; TITLE OF INVENTION: Detection Of Bovine Herpesvirus  
; TITLE OF INVENTION: Type 1  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hoffmann & Baron  
; STREET: 350 Jericho Turnpike  
; CITY: Jericho  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 11753  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette - 3.5 inch,  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: MS DOS  
; SOFTWARE: WORD PERFECT 6.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/150,203A  
; FILING DATE: December 6, 1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA: No. 5676951e  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Louise A. Foutch  
; REGISTRATION NUMBER: 37,133  
; REFERENCE/DOCKET NUMBER: 294-22  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 822-3550  
; TELEFAX: (516) 822-3582  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 284 nucleotides  
; TYPE: nucleotide  
; STRANDEDNESS: single  
; TOPOLOGY: Linear  
; US-08-150-203A-2

Query Match 30.0%; Score 18; DB 1; Length 284;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



```
QY 41 CCGACACGCGCCCGCTC 58
    |||||
Db 99 CCGACACGCGCCCGCTC 116

RESULT 2
US-08-454-730-2
; Sequence 2, Application US/08454730
; Patent No. 5789177
; GENERAL INFORMATION:
; APPLICANT: Rijsewijk, Franciscus Antonius Maria
; APPLICANT: van Oirschot, Johannes Theodorus
; APPLICANT: Maes, Roger Kamiel
; TITLE OF INVENTION: Bovine Herpesvirus Type 1
; TITLE OF INVENTION: Deletion Mutants, Vaccines Based
; TITLE OF INVENTION: Thereon, Diagnostic Kits For
; TITLE OF INVENTION: Detection Of Bovine Herpesvirus
; TITLE OF INVENTION: Type 1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann & Baron
; STREET: 350 Jericho Turnpike
; CITY: Jericho
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11753
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch,
; MEDIUM TYPE: 1.44 MB Storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS DOS
; SOFTWARE: WORD PERFECT 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,730
; FILING DATE: May 31, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/150,203
; FILING DATE: December 6, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Ronald J. Baron
; REGISTRATION NUMBER: 29,281
; REFERENCE/DOCKET NUMBER: 294-22 DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 822-3550
; TELEFAX: (516) 822-3582
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 284 nucleotides, 94 amino acids
; TYPE: nucleotide and amino acid
; STRANDEDNESS: single
; TOPOLOGY: Linear
US-08-454-730-2

Query Match 30.0%; Score 18; DB 1; Length 284;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 CCGACACGCGCCCGCTC 58
    |||||
Db 99 CCGACACGCGCCCGCTC 116

RESULT 3
US-08-949-788-2
; Sequence 2, Application US/08949788
; Patent No. 6403097
; GENERAL INFORMATION:
; APPLICANT: Rijsewijk, Franciscus Antonius Maria
; APPLICANT: van Oirschot, Johannes Theodorus
; APPLICANT: Maes, Roger Kamiel
; TITLE OF INVENTION: Bovine Herpesvirus Type 1

QY 41 CCGACACGCGCCCGCTC 58
    |||||
Db 99 CCGACACGCGCCCGCTC 116

RESULT 4
US-08-344-833-1
; Sequence 1, Application US/08344833
; Patent No. 5874280
; GENERAL INFORMATION:
; APPLICANT: Keil, G nther
; TITLE OF INVENTION: Recombinant Bovine Herpesvirus
; TITLE OF INVENTION: vaccine
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Organon Teknika Corporation
; STREET: 1330-A Piccard Drive
; CITY: Rockville
; STATE: Maryland
; COUNTRY: U.S.A.
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,833
```



```

; FILING DATE: 424
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Blackstone, William B.
; REGISTRATION NUMBER: 29.772
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 258-5200
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1289 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bovine herpesvirus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 142..1095
; OTHER INFORMATION: /product= "Protein"
; OTHER INFORMATION: /standard_name= "ORF-1"
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: 1..3
; OTHER INFORMATION: /function= "stop-codon giv"
; FEATURE:
; NAME/KEY: misc_RNA
; LOCATION: 4..141
; OTHER INFORMATION: /function= "untranslated"
; OTHER INFORMATION: region"
US-08-344-833-1

Query Match 30.0%; Score 18; DB 2; Length 1289;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 CCGACACGCGCCCGCTC 58
DB 461 CCGACACGCGCCCGCTC 478

RESULT 5
US-08-924-345-1
; Sequence 1, Application US/08924345
; Patent No. 6224878
; GENERAL INFORMATION:
; APPLICANT: LEUNG-TACK Patricia
; APPLICANT: LEGASTELOIS Isabelle, Christine, Marie-Andree
; APPLICANT: AUDONNET Jean-Christophe, Francis
; APPLICANT: RIVIERE Michel, Emile, Albert
; TITLE OF INVENTION: Mutants and vaccines of the Infectious
; TITLE OF INVENTION: Bovine Rhinotracheitis virus
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LARSON AND TAYLOR
; STREET: 727 SOUTH TWENTY-THIRD STREET
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/924,345
; FILING DATE: 04-SEP-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/199,172

```

```

; FILING DATE: 09-AUG-1994
; APPLICATION NUMBER: FR 92 07930
; FILING DATE: 26-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: SARRO, THOMAS P.
; REGISTRATION NUMBER: 19396
; REFERENCE/DOCKET NUMBER: XI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 920-7200
; TELEFAX: (703) 892-8428
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4190 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Type 1 Bovine Herpesvirus
; STRAIN: ST
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 172..1311
; OTHER INFORMATION: /function= "envelope glycoprotein"
; OTHER INFORMATION: /product= "glycoprotein gi"
; OTHER INFORMATION: /standard_name= "BHV-1 gi"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1594..3318
; OTHER INFORMATION: /function= "envelop glycoprotein"
; OTHER INFORMATION: /product= "glycoprotein gE"
; OTHER INFORMATION: /standard_name= "BHV-1 gE"
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3388..3861
; OTHER INFORMATION: /product= "protein US9"
; OTHER INFORMATION: /standard_name= "BHV US9"
US-08-924-345-1

Query Match 30.0%; Score 18; DB 3; Length 4190;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 CCGACACGCGCCCGCTC 58
DB 491 CCGACACGCGCCCGCTC 508

RESULT 6
US-09-252-991A-8962
; Sequence 8962, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8962
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8962

Query Match 28.3%; Score 17; DB 4; Length 1110;

```

```

Best Local Similarity 100.0%; Pred. No. 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 CGGCGCCCGACGCGC 51
    |||||
Db 189 CGGCGCCCGACGCGC 205

RESULT 7
US-09-252-991A-9043/c
; Sequence 9043, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9043
; LENGTH: 1278
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9043

Query Match 28.3%; Score 17; DB 4; Length 1278;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 CGGCGCCCGACGCGC 51
    |||||
Db 1154 CGGCGCCCGACGCGC 1138

RESULT 8
US-09-252-991A-8743
; Sequence 8743, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8743
; LENGTH: 1968
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8743

Query Match 28.3%; Score 17; DB 4; Length 1968;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 CGGCGCCCGACGCGC 51
    |||||
Db 875 CGGCGCCCGACGCGC 891

RESULT 9
US-09-036-987A-1/c
; Sequence 1, Application US/09036987A

```

```

; Patent No. 6143526
; GENERAL INFORMATION:
; APPLICANT: Baltz, Richard H.
; APPLICANT: Broughton, Mary C.
; APPLICANT: Crawford, Kathryn P.
; APPLICANT: Madduri, Krishnamurthy
; APPLICANT: Merlo, Donald J.
; APPLICANT: Treadway, Patti J.
; APPLICANT: Turner, Jan R.
; APPLICANT: Waldron, Clive
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
; TITLE OF INVENTION: Production
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dow Agrosciences LLC Patent Department
; STREET: 9330 Zionsville Road
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/036,987A
; FILING DATE: 09-MAR-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stuart, Donald R
; REGISTRATION NUMBER: 28,479
; REFERENCE/DOCKET NUMBER: 50,608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317)337-4816
; TELEFAX: (317)337-4847
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80161 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-036-987A-1

Query Match 28.3%; Score 17; DB 3; Length 80161;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CGCGCCGCTGCGCAG 25
    |||||
Db 22486 CGCGCCGCTGCGCAG 22470

RESULT 10
US-09-370-700-1/c
; Sequence 1, Application US/09370700
; Patent No. 6274350
; GENERAL INFORMATION:
; APPLICANT: Baltz, Richard H
; APPLICANT: Broughton, Mary C
; APPLICANT: Crawford, Kathryn P
; APPLICANT: Madduri, Krishnamurthy
; APPLICANT: Treadway, Patti J
; APPLICANT: Turner, Jan R
; APPLICANT: Waldron, Clive
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
; FILE REFERENCE: 50489 DIV1
; CURRENT APPLICATION NUMBER: US/09/370,700
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: US 09/36987
; EARLIER FILING DATE: 1998-03-09
; NUMBER OF SEQ ID NOS: 39

```

```
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 80161
; TYPE: DNA
; ORGANISM: Saccharopolyspora spinosa
US-09-370-700-1

Query Match      28.3%; Score 17; DB 3; Length 80161;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CGCGCCGCGCTGCGCAGC 25
Db 22486 CGCGCCGCGCTGCGCAGC 22470

RESULT 11
US-09-603-207-1/c
; Sequence 1, Application US/09603207B
; Patent No. 6521406
; GENERAL INFORMATION:
; APPLICANT: Baltz, Richard H
; APPLICANT: Broughton, Mary C
; APPLICANT: Crawford, Kathryn P
; APPLICANT: Madduri, Krishnamurthy
; APPLICANT: Treadway, Patti J
; APPLICANT: Turner, Jan R
; APPLICANT: Waldron, Clive
; TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
; FILE REFERENCE: 50489 DIV1
; CURRENT APPLICATION NUMBER: US/09/603,207B
; CURRENT FILING DATE: 2000-06-23
; EARLIER APPLICATION NUMBER: 09/370,700
; EARLIER FILING DATE: 1998-03-09
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 80161
; TYPE: DNA
; ORGANISM: Saccharopolyspora spinosa
US-09-603-207-1

Query Match      28.3%; Score 17; DB 4; Length 80161;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CGCGCCGCGCTGCGCAGC 25
Db 22486 CGCGCCGCGCTGCGCAGC 22470

RESULT 12
US-09-396-196G-98221
; Sequence 98221, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 98221
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-98221

Query Match      26.7%; Score 16; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CCTGCGCACGGAGTGA 31
Db 6 CCTGCGCACGGAGTGA 21

RESULT 13
US-09-396-196G-98222
; Sequence 98222, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 98222
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-98222

Query Match      26.7%; Score 16; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 CCTGCGCACGGAGTGA 31
Db 3 CCTGCGCACGGAGTGA 18

RESULT 14
US-09-902-540-4050/c
; Sequence 4050, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 4050
; LENGTH: 327
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-4050

Query Match      26.7%; Score 16; DB 4; Length 327;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ACCGCGCCGCGCTGCGC 22
Db 235 ACCGCGCCGCGCTGCGC 220
```

RESULT 15  
 US-09-252-991A-12729  
 ; Sequence 12729, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 107196.136  
 ; CURRENT APPLICATION NUMBER: US/09/252,991A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO 12729  
 ; LENGTH: 1122  
 ; TYPE: DNA  
 ; ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-12729

Query Match 26.7%; Score 16; DB 4; Length 1122;  
 Best Local Similarity 100.0%; Pred. No. 52;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GCGCCGCCTGCGCAG 25  
 |||||  
 Db 1081 GCGCCGCCTGCGCAG 1096

Search completed: June 30, 2005, 04:03:43  
 Job time : 121.2 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 29, 2005, 23:23:45 ; Search time 230.7 Seconds  
(without alignments)  
1625.622 Million cell updates/sec

Title: US-10-057-136-5  
Perfect score: 60  
Sequence: 1 ggatccacgcgcgcgtgc.....ccgacacgccccgctccc 60

Scoring table: OLIGO NUC  
Gapop: 60:0:0, Gapext 60.0

Searched: 6067389 seqs, 3125258755 residues

Word size : 0

Total number of hits satisfying chosen parameters: 12134778

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA:  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:  
9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:  
13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:  
14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:  
15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:  
16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:  
17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:  
18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:  
19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq:  
20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq:  
21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq:  
22: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:  
23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq:  
24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:  
25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:  
26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	60	100.0	60	14	US-10-057-136-5
2	60	100.0	2297	17	US-10-406-317-41
3	21	35.0	1523	18	US-10-425-114-13416
4	21	35.0	1805	19	US-10-437-963-15539
5	18	30.0	237	11	US-09-864-408A-3271
6	18	30.0	552	19	US-10-767-701-20454
7	17	28.3	403	20	US-10-425-115-125389
					Sequence 5, Appli
					Sequence 41, Appl
					Sequence 13416, A
					Sequence 15539, A
					Sequence 3271, Ap
					Sequence 20454, A
					Sequence 125389,

Query Match

100.0%; Score 60; DB 14; Length 60;

ALIGNMENTS

RESULT 1

US-10-057-136-5  
; Sequence 5, Application US/10057136  
; Publication No. US20030021770A1  
; GENERAL INFORMATION:  
; APPLICANT: SCHLOM, JEFFREY  
; APPLICANT: KANTOR, JUDITH  
; APPLICANT: KUFU, DONALD  
; APPLICANT: PANICALI, DENNIS  
; APPLICANT: GRITZ, LINDA  
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1  
; TITLE OF INVENTION: TUMOR-ASSOCIATED ANTIGEN  
; FILE REFERENCE: 700953/47113C  
; CURRENT APPLICATION NUMBER: US/10/057,136  
; CURRENT FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: 09/366,670  
; PRIOR FILING DATE: 1999-08-03  
; PRIOR APPLICATION NUMBER: PCT/US98/03693  
; PRIOR FILING DATE: 1998-02-24  
; PRIOR APPLICATION NUMBER: 60/038,253  
; PRIOR FILING DATE: 1997-02-24  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 60  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-057-136-5

8	17	28.3	556	20	US-10-425-115-79825	Sequence 79825, A
9	17	28.3	669	20	US-10-739-930-5219	Sequence 5219, Ap
10	17	28.3	807	20	US-10-472-260-159	Sequence 159, App
11	17	28.3	864	17	US-10-282-122A-13300	Sequence 13300, A
12	17	28.3	897	21	US-10-928-992-89	Sequence 89, Appl
13	17	28.3	1017	17	US-10-369-493-40005	Sequence 40005, A
14	17	28.3	1181	19	US-10-437-963-54065	Sequence 54065, A
15	17	28.3	1356	15	US-10-128-714-2220	Sequence 2220, Ap
16	17	28.3	1362	15	US-10-128-714-7220	Sequence 7220, Ap
17	17	28.3	1411	15	US-10-128-714-1220	Sequence 1220, Ap
18	17	28.3	1411	15	US-10-128-714-6220	Sequence 6220, Ap
19	17	28.3	3411	15	US-10-128-714-220	Sequence 220, App
20	17	28.3	3411	15	US-10-128-714-5220	Sequence 5220, Ap
21	17	28.3	80161	17	US-10-329-148A-1	Sequence 1, Appli
22	16	26.7	25	21	US-10-809-189-98221	Sequence 98221, A
23	16	26.7	25	21	US-10-809-189-98222	Sequence 98222, A
24	16	26.7	270	20	US-10-425-115-139852	Sequence 139852,
25	16	26.7	421	20	US-10-425-115-137245	Sequence 137245,
26	16	26.7	450	19	US-10-767-701-27455	Sequence 27455, A
27	16	26.7	546	19	US-10-437-963-30788	Sequence 30788, A
28	16	26.7	569	13	US-10-027-632-140046	Sequence 140046,
29	16	26.7	569	17	US-10-027-632-140046	Sequence 140046,
30	16	26.7	608	19	US-10-767-701-4719	Sequence 4719, Ap
31	16	26.7	668	19	US-10-437-963-81255	Sequence 81255, A
32	16	26.7	828	15	US-10-156-761-5770	Sequence 5770, Ap
33	16	26.7	1098	19	US-10-437-963-14713	Sequence 14713, A
34	16	26.7	1224	19	US-10-437-963-5514	Sequence 5514, Ap
35	16	26.7	1273	18	US-10-425-114-29003	Sequence 29003, A
36	16	26.7	1278	17	US-10-282-122A-25490	Sequence 25490, A
37	16	26.7	1342	19	US-10-767-701-7398	Sequence 7398, Ap
38	16	26.7	1374	15	US-10-156-761-5020	Sequence 5020, Ap
39	16	26.7	1437	20	US-10-425-115-106474	Sequence 106474,
40	16	26.7	1571	19	US-10-437-963-16579	Sequence 16579, A
41	16	26.7	1696	17	US-10-353-690-69	Sequence 69, Appl
42	16	26.7	1696	21	US-10-956-157-1776	Sequence 1776, Ap
43	16	26.7	1779	17	US-10-354-437-49	Sequence 49, Appl
44	16	26.7	1833	17	US-10-282-122A-27626	Sequence 27626, A
45	16	26.7	1911	17	US-10-282-122A-29194	Sequence 29194, A

Best Local Similarity 100.0%; Pred. No. 5.1e-24;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATCCACCGCGCGCCTGCGCACGGAGTGACGTGGCGCCGACACACGCGCCCGCTCCC 60  
Db 1 GGATCCACCGCGCGCCTGCGCACGGAGTGACGTGGCGCCGACACACGCGCCCGCTCCC 60

RESULT 2  
US-10-406-317-41  
; Sequence 41, Application US/10406317  
; Publication No. US20040019195A1  
; GENERAL INFORMATION:  
; APPLICANT: Schlom, Jeffrey;  
; APPLICANT: Hodge, James;  
; APPLICANT: Panicali, Dennis  
; TITLE OF INVENTION: A recombinant vector expressing multiple constimulatory  
; TITLE OF INVENTION: molecules and uses thereof  
; FILE REFERENCE: 38163-0189  
; CURRENT APPLICATION NUMBER: US/10/406,317  
; CURRENT FILING DATE: 2003-04-04  
; PRIOR APPLICATION NUMBER: US/09/856,988  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: PCT/US99/26866  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/111,582  
; PRIOR FILING DATE: 1998-12-09  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 41  
; LENGTH: 2297  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: VECTOR  
US-10-406-317-41

Query Match 100.0%; Score 60; DB 17; Length 2297;  
Best Local Similarity 100.0%; Pred. No. 2.2e-24;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATCCACCGCGCGCCTGCGCACGGAGTGACGTGGCGCCGACACACGCGCCCGCTCCC 60  
Db 466 GGATCCACCGCGCGCCTGCGCACGGAGTGACGTGGCGCCGACACACGCGCCCGCTCCC 525

RESULT 3  
US-10-425-114-13416  
; Sequence 13416, Application US/10425114  
; Publication No. US2004003488A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 13416  
; LENGTH: 1523  
; TYPE: DNA  
; ORGANISM: Oryza sativa nipponbare  
; FEATURE:  
; OTHER INFORMATION: Clone ID: JC-OSROLIB3475049G05\_FLI  
US-10-425-114-13416

Query Match 35.0%; Score 21; DB 18; Length 1523;

Best Local Similarity 100.0%; Pred. No. 0.024;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 GTGACGTCGGCGCCCGACACG 48  
Db 1074 GTGACGTCGGCGCCCGACACG 1094

RESULT 4  
US-10-437-963-15539  
; Sequence 15539, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 15539  
; LENGTH: 1805  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_21374C.1  
US-10-437-963-15539

Query Match 35.0%; Score 21; DB 19; Length 1805;  
Best Local Similarity 100.0%; Pred. No. 0.024;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 GTGACGTCGGCGCCCGACACG 48  
Db 1356 GTGACGTCGGCGCCCGACACG 1376

RESULT 5  
US-09-864-408A-3271/C  
; Sequence 3271, Application US/09864408A  
; Publication No. US20040009474A1  
; GENERAL INFORMATION:  
; APPLICANT: Leach, Martin D.  
; APPLICANT: Shimkets, Richard A.  
; TITLE OF INVENTION: No. US20040009474A1 Human Polynucleotides and Polypeptides Enco  
; FILE REFERENCE: 21402-012.  
; CURRENT APPLICATION NUMBER: US/09/864,408A  
; CURRENT FILING DATE: 2001-05-24  
; PRIOR APPLICATION NUMBER: 60/206,690  
; PRIOR FILING DATE: 2000-05-24  
; NUMBER OF SEQ ID NOS: 9068  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 3271  
; LENGTH: 237  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-864-408A-3271

Query Match 30.0%; Score 18; DB 11; Length 237;  
Best Local Similarity 100.0%; Pred. No. 1.9;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCGCGCGCGCTGCGCACG 25  
Db 213 CCGCGCGCGCTGCGCACG 196

```
RESULT 6
US-10-767-701-20454/c
; Sequence 20454, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 20454
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(552)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: LIB5121-012-A1-PF1-C3
US-10-767-701-20454
Query Match 30.0%; Score 18; DB 19; Length 552;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 GCCGACACGCGCCCGC 56
Db 301 GCCGACACGCGCCCGC 284

RESULT 7
US-10-425-115-125389/c
; Sequence 125389, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 125389
; LENGTH: 403
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_45827C.1
US-10-425-115-125389
Query Match 28.3%; Score 17; DB 20; Length 403;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 CGTCGGCGCCCGACACG 48
Db 155 CGTCGGCGCCCGACACG 139

RESULT 8
US-10-425-115-79825
; Sequence 79825, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: MICROBIOLOGICAL RESEARCH AUTHORITY
; APPLICANT: IMPERIAL COLLEGE INNOVATIONS LIMITED
; TITLE OF INVENTION: IMMUNOGENIC COMMENSAL NEISSERIA SEQUENCES
; FILE REFERENCE: GWS/DJC/23480
```

```
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 79825
; LENGTH: 556
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(556)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_172826C.1
US-10-425-115-79825
Query Match 28.3%; Score 17; DB 20; Length 556;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 TGACGTCGCGCCCGAC 45
Db 261 TGACGTCGCGCCCGAC 277

RESULT 9
US-10-739-930-5219/c
; Sequence 5219, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 5219
; LENGTH: 669
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(669)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: TRIAE-23APR03-CLUSTER681618_1
US-10-739-930-5219
Query Match 28.3%; Score 17; DB 20; Length 669;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATCCACCGCGCCGCC 17
Db 628 GGATCCACCGCGCCGCC 612

RESULT 10
US-10-472-260-159/c
; Sequence 159, Application US/10472260
; Publication No. US20040265328A1
; GENERAL INFORMATION:
; APPLICANT: MICROBIOLOGICAL RESEARCH AUTHORITY
; APPLICANT: IMPERIAL COLLEGE INNOVATIONS LIMITED
; TITLE OF INVENTION: IMMUNOGENIC COMMENSAL NEISSERIA SEQUENCES
; FILE REFERENCE: GWS/DJC/23480
```



; CURRENT APPLICATION NUMBER: US/10/472,260  
 ; CURRENT FILING DATE: 2003-09-22  
 ; NUMBER OF SEQ ID NOS: 199  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 159  
 ; LENGTH: 807  
 ; TYPE: DNA  
 ; ORGANISM: Neisseria meningitidis (group B)  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(807)  
 ; OTHER INFORMATION: shikimate-5-dehydrogenase  
 US-10-472-260-159

Query Match 28.3%; Score 17; DB 20; Length 807;  
 Best Local Similarity 100.0%; Pred. No. 5.1;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 CACCGCGCGCTGCGC 22  
 |||||  
 Db 405 CACCGCGCGCTGCGC 389

RESULT 11  
 US-10-282-122A-13300/c  
 ; Sequence 13300, Application US/10282122A  
 ; Publication No. US20040029129A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, Liangsu  
 ; APPLICANT: Zamudio, Carlos  
 ; APPLICANT: Malone, Cheryl  
 ; APPLICANT: Haselbeck, Robert  
 ; APPLICANT: Ohlsen, Kari  
 ; APPLICANT: Zyskind, Judith  
 ; APPLICANT: Wall, Daniel  
 ; APPLICANT: Trawick, John  
 ; APPLICANT: Carr, Grant  
 ; APPLICANT: Yamamoto, Robert  
 ; APPLICANT: Forsyth, R.  
 ; APPLICANT: Xu, H.  
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
 ; FILE REFERENCE: ELITRA.034A  
 ; CURRENT APPLICATION NUMBER: US/10/282,122A  
 ; CURRENT FILING DATE: 2003-02-20  
 ; PRIOR APPLICATION NUMBER: 60/191,078  
 ; PRIOR FILING DATE: 2000-03-21  
 ; PRIOR APPLICATION NUMBER: 60/206,848  
 ; PRIOR FILING DATE: 2000-05-23  
 ; PRIOR APPLICATION NUMBER: 60/207,727  
 ; PRIOR FILING DATE: 2000-05-26  
 ; PRIOR APPLICATION NUMBER: 60/230,335  
 ; PRIOR FILING DATE: 2000-09-06  
 ; PRIOR APPLICATION NUMBER: 60/230,347  
 ; PRIOR FILING DATE: 2000-09-09  
 ; PRIOR APPLICATION NUMBER: 60/242,578  
 ; PRIOR FILING DATE: 2000-10-23  
 ; PRIOR APPLICATION NUMBER: 60/253,625  
 ; PRIOR FILING DATE: 2000-11-27  
 ; PRIOR APPLICATION NUMBER: 60/257,931  
 ; PRIOR FILING DATE: 2000-12-22  
 ; PRIOR APPLICATION NUMBER: 60/267,636  
 ; PRIOR FILING DATE: 2001-02-09  
 ; PRIOR APPLICATION NUMBER: 60/269,308  
 ; PRIOR FILING DATE: 2001-02-16  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 78614  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 13300  
 ; LENGTH: 864  
 ; TYPE: DNA  
 ; ORGANISM: Burkholderia fungorum  
 US-10-282-122A-13300

Query Match 28.3%; Score 17; DB 17; Length 864;  
 Best Local Similarity 100.0%; Pred. No. 5;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GATCCACCGCGCGCT 18  
 |||||  
 Db 808 GATCCACCGCGCGCT 792  
 |||||  
 RESULT 12  
 US-10-928-992-89/c  
 ; Sequence 89, Application US/10928992  
 ; Publication No. US20050097639A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Nguyen, Henry T  
 ; APPLICANT: Kreps, Joel A  
 ; TITLE OF INVENTION: NUCLEIC ACID MOLECULES FROM RICE CONTROLLING ABIOTIC STRESS  
 ; TITLE OF INVENTION: TOLERANCE  
 ; FILE REFERENCE: 1392/8/2  
 ; CURRENT APPLICATION NUMBER: US/10/928,992  
 ; CURRENT FILING DATE: 2004-08-27  
 ; PRIOR APPLICATION NUMBER: US 60/498,183  
 ; PRIOR FILING DATE: 2003-08-27  
 ; NUMBER OF SEQ ID NOS: 198  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 89  
 ; LENGTH: 897  
 ; TYPE: DNA  
 ; ORGANISM: Oryza sativa  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(897)  
 US-10-928-992-89

Query Match 28.3%; Score 17; DB 21; Length 897;  
 Best Local Similarity 100.0%; Pred. No. 5;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 TCCACCGCGCGCTGC 20  
 |||||  
 Db 217 TCCACCGCGCGCTGC 201  
 |||||

RESULT 13  
 US-10-369-493-40005  
 ; Sequence 40005, Application US/10369493  
 ; Publication No. US20030233675A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Hinkle, Gregory J.  
 ; APPLICANT: Slater, Steven C.  
 ; APPLICANT: Goldman, Barry S.  
 ; APPLICANT: Chen, Xianfeng  
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
 ; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
 ; FILE REFERENCE: 38-10(52052)B  
 ; CURRENT APPLICATION NUMBER: US/10/369,493  
 ; CURRENT FILING DATE: 2003-02-28  
 ; PRIOR APPLICATION NUMBER: US 60/360,039  
 ; PRIOR FILING DATE: 2002-02-21  
 ; NUMBER OF SEQ ID NOS: 47374  
 ; SEQ ID NO 40005  
 ; LENGTH: 1017  
 ; TYPE: DNA  
 ; ORGANISM: Xanthomonas campestris  
 US-10-369-493-40005

Query Match 28.3%; Score 17; DB 17; Length 1017;  
 Best Local Similarity 100.0%; Pred. No. 4.9;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 ACCGCGCGCGCTGCGCA 23  
 |||||



Db 873 ACCGGCGCGCTGCGCA 889

## RESULT 14

US-10-437-963-54065/c  
; Sequence 54065, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 54065  
; LENGTH: 1181  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_56204C.1  
US-10-437-963-54065

Query Match 28.3%; Score 17; DB 19; Length 1181;  
Best Local Similarity 100.0%; Pred. No. 4.7;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCCACCGCGCGCCTGC 20  
|||||  
Db 317 TCCACCGCGCGCCTGC 301

## RESULT 15

US-10-128-714-2220/c  
; Sequence 2220, Application US/10128714  
; Publication No. US20030119013A1  
; GENERAL INFORMATION:  
; APPLICANT: Jiang, Bo  
; APPLICANT: Hu, Wenqi  
; APPLICANT: Tishkoff, Daniel  
; APPLICANT: Zamudio, Carlos  
; APPLICANT: Eroshkin, Alexey M  
; APPLICANT: Lemieux, Sebastien M  
; TITLE OF INVENTION: Identification of Essential Genes in *Aspergillus fumigatus* and  
; TITLE OF INVENTION: Methods of Use  
; FILE REFERENCE: 10182-018-999  
; CURRENT APPLICATION NUMBER: US/10/128,714  
; CURRENT FILING DATE: 2002-04-23  
; PRIOR APPLICATION NUMBER: US 60/285,697  
; PRIOR FILING DATE: 2001-04-23  
; PRIOR APPLICATION NUMBER: US 60/287,066  
; PRIOR FILING DATE: 2001-04-27  
; PRIOR APPLICATION NUMBER: US 60/295,890  
; PRIOR FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: US 60/303,899  
; PRIOR FILING DATE: 2001-07-09  
; PRIOR APPLICATION NUMBER: US 60/316,362  
; PRIOR FILING DATE: 2001-08-31  
; NUMBER OF SEQ ID NOS: 8603  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2220  
; LENGTH: 1356  
; TYPE: DNA  
; ORGANISM: *Aspergillus fumigatus*  
US-10-128-714-2220

Query Match 28.3%; Score 17; DB 15; Length 1356;  
Best Local Similarity 100.0%; Pred. No. 4.5;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCACCGCGCGCCTGCG 21  
|||||  
Db 468 CCACCGCGCGCCTGCG 452

Search completed: June 30, 2005, 04:42:38  
Job time : 398.7 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 30, 2005, 06:50:10 ; Search time 2133 Seconds  
(without alignments)  
356.908 Million cell updates/sec

Title: US-10-057-136-1

Perfect score: 109

Sequence: 1 GSTAPPAHGVTSPDTRPAP 20

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/cgn2 1/USPTO spool/US10057136/runat 29062005 162123 11398/app query.fasta 1.199  
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -IOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10057136 @CGN 1 1 3437 @runat 29062005 162123 11398 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_htc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	109	100.0	330	1 AI925867	AI925867 wo20d04.x
2	109	100.0	604	4 BM791359	BM791359 K-EST0071
3	109	100.0	877	5 BU542454	BU542454 AGENCOURT
4	109	100.0	959	6 CA489836	CA489836 AGENCOURT
5	109	100.0	1113	5 BU148487	BU148487 AGENCOURT
6	109	100.0	1130	5 BU542996	BU542996 AGENCOURT
7	109	100.0	1234	5 BQ936898	BQ936898 AGENCOURT
8	109	100.0	1262	5 BQ935496	BQ935496 AGENCOURT
9	109	100.0	1268	5 BQ943554	BQ943554 AGENCOURT

10	109	100.0	1343	5	BQ920055	BQ920055 AGENCOURT
11	109	100.0	1349	5	BU152566	BU152566 AGENCOURT
12	109	100.0	1420	5	BU542790	BU542790 AGENCOURT
13	109	100.0	1531	5	BU543309	BU543309 AGENCOURT
14	97	89.0	981	4	BG774910	BG774910 602649832
15	97	89.0	1536	5	BQ923149	BQ923149 AGENCOURT
16	91	83.5	475	6	CB120860	CB120860 K-EST0168
17	91	83.5	669	6	CB122585	CB122585 K-EST0170
18	91	83.5	1334	5	BQ943809	BQ943809 AGENCOURT
19	90	82.6	472	4	BM759495	BM759495 K-EST0039
20	88	80.7	166	7	T27692	T27692 EST12384 Hu
21	83	76.1	619	4	BI260921	BI260921 602970962
22	83	76.1	1678	4	BG775565	BG775565 602650481
C 23	64	58.7	926	4	BI754598	BI754598 603025144
C 24	62	56.9	451	4	BG724943	BG724943 EtESTed43
C 25	62	56.9	465	4	BG724531	BG724531 EtESTed90
26	62	56.9	705	9	AG043162	AG043162 Pan trogl
27	62	56.9	760	7	CO565665	CO565665 AGENCOURT
28	62	56.9	969	5	BU221571	BU221571 603105394
C 29	62	56.9	2448	9	CG756594	CG756594 P051-4-CO
30	61	56.0	418	7	CN138277	CN138277 OX1 62 GO
31	61	56.0	510	9	CC719180	CC719180 OGDE05TC
C 32	61	56.0	665	9	CC701843	CC701843 OGMAP95TV
33	61	56.0	756	9	CC701830	CC701830 OGMAP95TH
C 34	61	56.0	773	9	CG217984	CG217984 OG0G137TH
C 35	61	56.0	818	8	BZ713938	BZ713938 OGCDI62TC
C 36	61	56.0	838	8	BZ534307	BZ534307 OGALD67TC
C 37	61	56.0	839	9	CG372937	CG372937 OG0CO84TH
C 38	61	56.0	928	9	CG260788	CG260788 OG1BG20TV
39	61	56.0	1049	9	CNS07685	AL431090 T3 end of
40	61	56.0	1339	8	CC191632	CC191632 CH261-6L1
C 41	61	56.0	1343	9	AG185838	AG185838 Pan trogl
42	60.5	55.5	1276	4	BG328273	BG328273 602427706
43	60.5	55.5	1712	4	BG111464	BG111464 602282966
44	60	55.0	445	9	CL928152	CL928152 OA ABa003
45	60	55.0	637	9	AG093550	AG093550 Pan trogl

ALIGNMENTS

RESULT 1

AI925867/c

LOCUS

DEFINITION

AI925867 330 bp mRNA linear EST 08-MAR-2000  
wo20d04.x1 NCI CGAP Panl Homo sapiens cDNA clone IMAGE:2455879 3'  
similar to contains element MSR1 MSR1 repetitive element ;, mRNA  
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AI925867.1 GI:5661831  
EST.  
Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 330)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP).

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Life Technologies catalog #: 11548-013

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Insert Length: 578 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 305.

Location/Qualifiers

1. .330

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

FEATURES

source

```
/clone="IMAGE:2455879"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI CGAP_Pan1"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"

ORIGIN
Alignment Scores:
Pred. No.: 0.000595 Length: 330
Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-057-136-1 (1-20) x AI925867 (1-330)

QY 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
|||||
Db 316 GGCTCCACCGCCCCCAGCCACGGTGTCACCTCGGCCCGGACACACAGCGGCCCG 257

RESULT 2
BM791359
LOCUS BM791359 604 bp mRNA linear EST 05-MAR-2002
DEFINITION K-EST0071342 S21SNU520 Homo sapiens cDNA clone S21SNU520-14-A06 5',
mRNA sequence.
ACCESSION BM791359
VERSION BM791359.1 GI:19139591
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 604)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 14 row: A column: 06
High quality sequence stop: 604.

FEATURES
source
Location/Qualifiers
1..604
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S21SNU520-14-A06"
/sex="F"
/tissue_type="Stomach"
/cell_type="Floating aggregates"
/cell_line="SNU-520"
/lab_host="Top10F"
/clone_lib="S21SNU520"
/note="Organ: Stomach; Vector: pTZ18RP1; Site 1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dT-selected mRNA by
priming with dT-tailed vector. The dT-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of

/clon="IMAGE:2455879"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI CGAP_Pan1"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"

ORIGIN
Alignment Scores:
Pred. No.: 0.00108 Length: 604
Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-057-136-1 (1-20) x BM791359 (1-604)

QY 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
|||||
Db 28 GGCTCCACCGCACCCCGCCAGCCACGGTGTCACCTCGGCCCGGACACACAGCGGCCCG 87

RESULT 3
BU542454
LOCUS BU542454 877 bp mRNA linear EST 13-SEP-2002
DEFINITION AGENCOURT_10322173 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:6574322
5', mRNA sequence.
ACCESSION BU542454
VERSION BU542454.1 GI:22852937
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 877)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM2769 row: h column: 02
High quality sequence stop: 760.

FEATURES
source
Location/Qualifiers
1..877
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6574322"
/tissue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_40"
/note="Organ: prostate; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 0.00155 Length: 877
Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
```

```
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-057-136-1 (1-20) x BU542454 (1-877)

QY 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
   |||||
Db 35 GGCTCCACCGCCCCCAGCCACGGGTGTACCTCGGCCCGGACACACCGAGCGGCCCG 94

RESULT 4
CA489836
LOCUS
DEFINITION AGENCOURT_10810668 MAPcL Homo sapiens cDNA clone image:6722324 5',
          mRNA sequence.
ACCESSION CA489836
VERSION CA489836.1 GI:24952627
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 959)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: Invitrogen Corp
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM14284 row: n column: 20
          High quality sequence start: 31
          High quality sequence stop: 446.

FEATURES
Source
1..959
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6722324"
/cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,
hTERT-HME1, LNCap"
/lab_host="EMDH10B"
/clone_lib="MAPcL"
/note="Vector: pCMV-SPORT6; Site 1: EcorV; Site 2: Not I;
Subtracted with brain, liver, lung, kidney and muscle.
Directionally cloned. Priming method: oligo-dr. Average
insert size: 1800 bp. Library amplification: 26,000 fold.
Kristi A. Eglund, James J. Vincent, Robert Strausberg,
Bungkook Lee & Ira Pastan: Discovery of new breast
cancer genes encoding membrane and secreted proteins.
Manuscript submitted."

ORIGIN
Alignment Scores:
Pred. No.: 0.00169 Length: 959
Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-057-136-1 (1-20) x CA489836 (1-959)

QY 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
   |||||
Db 349 GGCTCCACCGCCCCCAGCCACGGGTGTACCTCGGCCCGGACACACCGAGCGGCCCG 408

RESULT 5
BU148487

LOCUS
DEFINITION AGENCOURT_8670479 NIH_MGC_40 Homo sapiens cDNA clone image:6380642
          5', mRNA sequence.
ACCESSION BU148487
VERSION BU148487.1 GI:22662019
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1113)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-r@mail.nih.gov
          Tissue Procurement: DCTD/DTP
          cDNA Library Preparation: Rubin Laboratory
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLCM2569 row: j column: 03
          High quality sequence stop: 235.

FEATURES
Source
1..1113
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6380642"
/tissue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_40"
/note="Organ: prostate; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 0.00196 Length: 1113
Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-057-136-1 (1-20) x BU148487 (1-1113)

QY 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
   |||||
Db 30 GGCTCCACCGCCCCCAGCCACGGGTGTACCTCTGCCCCGGACACACCGAGCGGCCCG 89

RESULT 6
BU542996
LOCUS
DEFINITION AGENCOURT_10338707 NIH_MGC_40 Homo sapiens cDNA clone image:6574979
          5', mRNA sequence.
ACCESSION BU542996
VERSION BU542996.1 GI:22853479
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1130)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
```

JOURNAL COMMENT Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTP  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LCM2771 row: c column: 11  
High quality sequence start: 27  
High quality sequence stop: 246.

FEATURES source Location/Qualifiers  
1. .1130  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6574979"  
/tissue\_type="carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_40"  
/note="Organ: prostate; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

ORIGIN  
Alignment Scores:  
Pred. No.: 0.00199 Length: 1130  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservatative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 5 Gaps: 0

US-10-057-136-1 (1-20) x BU542996 (1-1130)

QY 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
|||||  
69 GGCTCCACCGCCCCCGACGCCACGGGTGCACCTCGGCCCGGACACCGCGGCCCG 128

RESULT 7  
BQ936898  
LOCUS BQ936898 1234 bp mRNA linear EST 21-AUG-2002  
DEFINITION AGENCOURT\_8919110 NIH\_MGC\_40 Homo sapiens cDNA clone IMAGE:6383855  
5', mRNA sequence.  
ACCESSION BQ936898  
VERSION BQ936898.1 GI:22352281  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1234)  
NIH-MGC http://mgi.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTP  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LCM2577 row: o column: 24  
High quality sequence stop: 245.

FEATURES source Location/Qualifiers  
1. .1234  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6383855"  
/tissue\_type="carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_40"  
/note="Organ: prostate; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

ORIGIN  
Alignment Scores:  
Pred. No.: 0.00217 Length: 1234  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservatative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 5 Gaps: 0

US-10-057-136-1 (1-20) x BQ936898 (1-1234)

QY 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
|||||  
30 GGCTCCACCGCCCCCGACGCCACGGGTGCACCTCTGCCCGGACACCGCGGCCCG 89

RESULT 8  
BQ935496  
LOCUS BQ935496 1262 bp mRNA linear EST 21-AUG-2002  
DEFINITION AGENCOURT\_8776475 NIH\_MGC\_40 Homo sapiens cDNA clone IMAGE:6382088  
5', mRNA sequence.  
ACCESSION BQ935496  
VERSION BQ935496.1 GI:22350879  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1262)  
NIH-MGC http://mgi.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTP  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LCM2573 row: f column: 09  
High quality sequence start: 46  
High quality sequence stop: 157.

FEATURES source Location/Qualifiers  
1. .1262  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6382088"  
/tissue\_type="carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_40"  
/note="Organ: prostate; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

ORIGIN

Alignment Scores:  
Pred. No.: 0.00222 Length: 1262  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 5 Gaps: 0

US-10-057-136-1 (1-20) x BQ935496 (1-1262)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
|||||  
Db 56 GGCTCCACCGCCCCCGACGCCACGGTGTACCTCTGCCCTGACACCGCGGCCCG 115

RESULT 9  
BQ943554 1268 bp mRNA linear EST 21-AUG-2002  
LOCUS AGENCOURT\_8777815 NIH\_MGC\_40 Homo sapiens cDNA clone IMAGE:6384308  
DEFINITION 5', mRNA sequence.

ACCESSION BQ943554  
VERSION BQ943554.1 GI:22359032  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1268)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-re@mail.nih.gov  
Tissue Procurement: DCTD/DTF  
cDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
Plate: LLCM2579 row: b column: 21  
High quality sequence stop: 177.

FEATURES

source  
1. .1268  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6384308"  
/tissue\_type="carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_40"  
/note="Organ: prostate; Vector: pOTB7; Site 1: XhoI;  
Site 2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

ORIGIN

Alignment Scores:  
Pred. No.: 0.00223 Length: 1268  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0

DB:

US-10-057-136-1 (1-20) x BQ943554 (1-1268)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
|||||  
Db 90 GGCTCCACCGCCCCCGACGCCACGGTGTACCTCGGCCCGGACACCGCGGCCCG 149

RESULT 10

BQ920055

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-re@mail.nih.gov

Tissue Procurement: DCTD/DTF

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: LLCM2663 row: e column: 02

High quality sequence start: 56

High quality sequence stop: 237.

Location/Qualifiers

1. .1343

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6481609"

/tissue\_type="carcinoma, cell line"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_40"

/note="Organ: prostate; Vector: pOTB7; Site 1: XhoI;  
Site 2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

ORIGIN

Alignment Scores:  
Pred. No.: 0.00236 Length: 1343  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 5 Gaps: 0

US-10-057-136-1 (1-20) x BQ920055 (1-1343)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
|||||  
Db 72 GGCTCCACCGCCCCCGACGCCACGGTGTACCTCTGCCCGGACACCGCGGCCCG 131

RESULT 11

BUI52566

LOCUS

DEFINITION

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-re@mail.nih.gov

Tissue Procurement: DCTD/DTF

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: LLCM2579 row: b column: 21

High quality sequence stop: 177.

Location/Qualifiers

1. .1268

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6384308"

/tissue\_type="carcinoma, cell line"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_40"

/note="Organ: prostate; Vector: pOTB7; Site 1: XhoI;  
Site 2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."



5', mRNA sequence.  
ACCESSION BU152566  
VERSION BU152566.1 GI:22666098  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 1349)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: DCTD/DTP  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLCM2569 row: f column: 16  
High quality sequence stop: 291.  
Location/Qualifiers  
1. .1349  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6380559"  
/tissue\_type="carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_40"  
/note="Organ: prostate; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."  
ORIGIN  
Alignment Scores:  
Pred. No.: 0.00237 Length: 1349  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 5 Gaps: 0  
US-10-057-136-1 (1-20) x BU152566 (1-1349)  
QY 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
Db 19 GGCTCCACCGCCCCCGCCAGCCCGGTGTCACTCGGCCCGGACACCGCGGCCCG 78  
RESULT 12  
BU542790  
LOCUS BU542790 1420 bp mRNA linear EST 13-SEP-2002  
DEFINITION AGENCOURT\_10334841 NIH\_MGC\_40 Homo sapiens cDNA clone IMAGE:6574725  
5', mRNA sequence.  
ACCESSION BU542790  
VERSION BU542790.1 GI:22853273  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 1420)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: DCTD/DTP  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLCM2770 row: b column: 21  
High quality sequence stop: 166.  
Location/Qualifiers  
1. .1531  
/organism="Homo sapiens"

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: DCTD/DTP  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLCM2770 row: h column: 21  
High quality sequence stop: 288.  
Location/Qualifiers  
1. .1420  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6574725"  
/tissue\_type="carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_40"  
/note="Organ: prostate; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."  
ORIGIN  
Alignment Scores:  
Pred. No.: 0.00249 Length: 1420  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 5 Gaps: 0  
US-10-057-136-1 (1-20) x BU542790 (1-1420)  
QY 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
Db 19 GGCTCCACCGCCCCCGCCAGCCCGGTGTCACTCGGCCCGGACACCGCGGCCCG 78  
RESULT 13  
BU543309  
LOCUS BU543309 1531 bp mRNA linear EST 13-SEP-2002  
DEFINITION AGENCOURT\_10327072 NIH\_MGC\_40 Homo sapiens cDNA clone IMAGE:6575349  
5', mRNA sequence.  
ACCESSION BU543309  
VERSION BU543309.1 GI:22853792  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 1531)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: DCTD/DTP  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLCM2772 row: b column: 21  
High quality sequence stop: 166.  
Location/Qualifiers  
1. .1531  
/organism="Homo sapiens"



/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6575349"  
/tissue\_type="carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_40"  
/note="Organ: prostate; Vector: pOTB7; Site 1: XhoI;  
Site 2: EcoRI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACGAG(G). Library constructed by  
Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

ORIGIN

Alignment Scores:  
Pred. No.: 0.00268 Length: 1531  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 5 Gaps: 0

US-10-057-136-1 (1-20) x BU543309 (1-1531)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
Db 30 GGCTCCACCGCCCGCCAGCCCGGTGTACCTGTCCCGGACACCGCCGCGCCCG 89

RESULT 14

BG774910 981 bp mRNA linear EST 15-MAY-2001  
LOCUS 602649832F1 NIH\_MGC\_40 Homo sapiens cDNA clone IMAGE:4761054 5',  
DEFINITION mRNA sequence.

ACCESSION BG774910

VERSION BG774910.1 GI:14045227

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 981)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1612 row: 0 column: 07

High quality sequence stop: 874.

Location/Qualifiers

1. .981

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4761054"

/tissue\_type="carcinoma, cell line"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_40"

/note="Organ: prostate; Vector: pOTB7; Site 1: XhoI;  
Site 2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACGAG(G). Library constructed by

Ling Hong in the laboratory of Gerald M. Rubin (University

of California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies).

ORIGIN

Alignment Scores:  
Pred. No.: 0.0524 Length: 981  
Score: 97.00 Matches: 18  
Percent Similarity: 94.74% Conservative: 0  
Best Local Similarity: 94.74% Mismatches: 1  
Query Match: 88.99% Indels: 0  
DB: 4 Gaps: 0

US-10-057-136-1 (1-20) x BG774910 (1-981)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAla 19  
Db 21 GGCTCCACCGCCCGCCAGCCCATGGTGTCTACCTCGGCCCGGACACAGCGCCGCC 77

RESULT 15

BQ923149

LOCUS BQ923149

DEFINITION AGENCOURT 8929207 NIH\_MGC\_40 Homo sapiens cDNA clone IMAGE:6484568

5', mRNA sequence.

ACCESSION BQ923149

VERSION BQ923149.1 GI:22338180

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1536)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2670 row: p column: 09

High quality sequence stop: 287.

Location/Qualifiers

1. .1536

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6484568"

/tissue\_type="carcinoma, cell line"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_40"

/note="Organ: prostate; Vector: pOTB7; Site 1: XhoI;  
Site 2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACGAG(G). Library constructed by

Ling Hong in the laboratory of Gerald M. Rubin (University

of California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH\_MGC Library."

ORIGIN

Alignment Scores:  
Pred. No.: 0.0814 Length: 1536  
Score: 97.00 Matches: 18  
Percent Similarity: 94.74% Conservative: 0  
Best Local Similarity: 94.74% Mismatches: 1  
Query Match: 88.99% Indels: 0  
DB: 5 Gaps: 0

US-10-057-136-1 (1-20) x BQ923149 (1-1536)

Qy 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAla 19  
Db 18 GGCTCCACCCGCCCCAGCCCATGGTGTACCTCGGCCCGGACAAACAGGCCCGCC 74

Search completed: June 30, 2005, 08:43:23  
Job time : 2143 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 30, 2005, 07:18:05 ; Search time 1601 Seconds  
(without alignments)  
78.353 Million cell updates/sec

Title: US-10-057-136-1

Perfect score: 109

Sequence: 1 GSTAPPAHGVTSPDTRPAP 20

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delopt 6.0 , Delext 7.0

Searched: 6313374 seqs, 3136092125 residues

Total number of hits satisfying chosen parameters: 12626748

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=xlh  
-O=/cgn2\_1/USPTO spool/US10057136/runat 29062005 162124 11430/app query.fasta\_1.199  
-DB=Published Applications NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US10057136 @CGN 1 1 480 @runat 29062005 162124 11430  
-NCFU=6 -ICPU=3 -NO\_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THEADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:  
1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*  
2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq.\*  
5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*  
8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*  
9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq.\*  
11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq.\*  
12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*  
13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq.\*  
14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq.\*  
15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq.\*  
16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq.\*  
17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq.\*  
18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq.\*  
19: /cgn2\_6/ptodata/2/pubpna/US10G\_PUBCOMB.seq.\*  
20: /cgn2\_6/ptodata/2/pubpna/US10H\_PUBCOMB.seq.\*  
21: /cgn2\_6/ptodata/2/pubpna/US10I\_PUBCOMB.seq.\*  
22: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*  
23: /cgn2\_6/ptodata/2/pubpna/US11A\_PUBCOMB.seq.\*  
24: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*  
25: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*  
26: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	109	100.0	60	14	US-10-057-136-2	Sequence 2, Appli
2	109	100.0	60	14	US-10-057-136-4	Sequence 4, Appli
3	109	100.0	60	14	US-10-057-136-5	Sequence 5, Appli
4	109	100.0	60	14	US-10-057-136-6	Sequence 6, Appli
5	109	100.0	60	14	US-10-057-136-7	Sequence 7, Appli
6	109	100.0	60	14	US-10-057-136-8	Sequence 8, Appli
7	109	100.0	60	14	US-10-057-136-9	Sequence 9, Appli
8	109	100.0	60	14	US-10-057-136-10	Sequence 10, Appli
9	109	100.0	60	14	US-10-057-136-11	Sequence 11, Appli
10	109	100.0	60	14	US-10-057-136-12	Sequence 12, Appli
11	109	100.0	120	21	US-10-635-211-3	Sequence 3, Appli
12	109	100.0	162	21	US-10-635-211-8	Sequence 8, Appli
13	109	100.0	1424	17	US-10-447-839A-75	Sequence 75, Appli
14	109	100.0	1424	21	US-10-778-859-75	Sequence 75, Appli
15	109	100.0	1428	17	US-10-447-839A-20	Sequence 20, Appli
16	109	100.0	1428	21	US-10-778-859-20	Sequence 20, Appli
17	109	100.0	1527	14	US-10-057-136-19	Sequence 19, Appli
18	109	100.0	1761	21	US-10-635-211-1	Sequence 1, Appli
19	109	100.0	1799	17	US-10-447-839A-19	Sequence 19, Appli
20	109	100.0	1799	21	US-10-778-859-19	Sequence 19, Appli
21	109	100.0	1804	9	US-09-964-824A-573	Sequence 573, App
22	109	100.0	1804	15	US-10-029-517-17	Sequence 17, Appli
23	109	100.0	1804	19	US-10-717-597-30	Sequence 30, Appli
24	109	100.0	1804	19	US-10-775-920-84	Sequence 84, Appli
25	109	100.0	1804	21	US-10-843-641A-5876	Sequence 5876, Ap
26	109	100.0	1823	15	US-10-101-510-339	Sequence 339, App
27	109	100.0	2297	17	US-10-406-317-41	Sequence 41, Appli
28	109	100.0	4139	9	US-09-964-824A-105	Sequence 105, App
29	109	100.0	4139	9	US-09-964-824A-578	Sequence 578, App
30	109	100.0	4139	9	US-09-864-864-334	Sequence 334, App
31	109	100.0	4139	9	US-09-880-107-2121	Sequence 2121, Ap
32	109	100.0	4139	11	US-09-968-007A-751	Sequence 751, App
33	109	100.0	4139	14	US-10-171-311-157	Sequence 157, App
34	109	100.0	4139	15	US-10-177-293-310	Sequence 310, App
35	109	100.0	4139	17	US-10-440-464-155	Sequence 155, App
36	109	100.0	4139	19	US-10-734-564-53	Sequence 53, Appli
37	109	100.0	4139	19	US-10-775-920-80	Sequence 80, Appli
38	109	100.0	4139	19	US-10-775-920-85	Sequence 85, Appli
39	109	100.0	4139	21	US-10-843-641A-5408	Sequence 5408, Ap
40	109	100.0	4139	21	US-10-843-641A-5881	Sequence 5881, Ap
41	109	100.0	4139	21	US-10-843-641A-7221	Sequence 7221, Ap
42	109	100.0	8181	11	US-09-951-938-18	Sequence 18, Appli
43	109	100.0	8181	17	US-10-447-839A-18	Sequence 18, Appli
44	109	100.0	8181	21	US-10-778-859-18	Sequence 18, Appli
45	109	100.0	8186	15	US-10-029-517-19	Sequence 19, Appli

ALIGNMENTS

RESULT 1

US-10-057-136-2  
; Sequence 2, Application US/10057136  
; Publication No. US20030021770A1  
; GENERAL INFORMATION:  
; APPLICANT: SCHLOM, JEFFREY  
; APPLICANT: KANTOR, JUDITH  
; APPLICANT: KUFE, DONALD  
; APPLICANT: PANICALI, DENNIS  
; APPLICANT: GRITZ, LINDA  
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1  
; TITLE OF INVENTION: TUMOR-ASSOCIATED ANTIGEN  
; FILE REFERENCE: 700953/47113C  
; CURRENT APPLICATION NUMBER: US/10/057,136  
; PRIOR APPLICATION DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: 09/366,670

```
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: PCT/US98/03693
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 60/038,253
; PRIOR FILING DATE: 1997-02-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-057-136-2

Alignment Scores:
Pred. No.: 3.04e-07 Length: 60
Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-057-136-1 (1-20) x US-10-057-136-2 (1-60)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db 1 GGCTCCACCGCCCCCAGCCACGGTGTCACTCGGCCCGGACACCCAGCGGCCCG 60

RESULT 2
US-10-057-136-4
; Sequence 4, Application US/10057136
; Publication No. US20030021770A1
; GENERAL INFORMATION:
; APPLICANT: SCHLOM, JEFFREY
; APPLICANT: KANTOR, JUDITH
; APPLICANT: KUFU, DONALD
; APPLICANT: PANICALI, DENNIS
; APPLICANT: GRITZ, LINDA
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1
; TITLE OF INVENTION: TUMOR-ASSOCIATED ANTIGEN
; FILE REFERENCE: 700953/47113C
; CURRENT APPLICATION NUMBER: US/10/057,136
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 09/366,670
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: PCT/US98/03693
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 60/038,253
; PRIOR FILING DATE: 1997-02-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-057-136-4

Alignment Scores:
Pred. No.: 3.04e-07 Length: 60
Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-057-136-1 (1-20) x US-10-057-136-4 (1-60)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db 1 GGCAGTACTGCACCGCCGACATGGCGTAACATCAGCACCTGATACAGACCTGCACCT 60

RESULT 3
US-10-057-136-5
; Sequence 5, Application US/10057136
```

```
; Publication No. US20030021770A1
; GENERAL INFORMATION:
; APPLICANT: SCHLOM, JEFFREY
; APPLICANT: KANTOR, JUDITH
; APPLICANT: KUFU, DONALD
; APPLICANT: PANICALI, DENNIS
; APPLICANT: GRITZ, LINDA
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1
; TITLE OF INVENTION: TUMOR-ASSOCIATED ANTIGEN
; FILE REFERENCE: 700953/47113C
; CURRENT APPLICATION NUMBER: US/10/057,136
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 09/366,670
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: PCT/US98/03693
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 60/038,253
; PRIOR FILING DATE: 1997-02-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-057-136-5

Alignment Scores:
Pred. No.: 3.04e-07 Length: 60
Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-057-136-1 (1-20) x US-10-057-136-5 (1-60)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db 1 GGATCCACCGCGCCCTCGCACGGAGTACGTGCGGCCCGGACACGCGCGCCGCTCCC 60

RESULT 4
US-10-057-136-6
; Sequence 6, Application US/10057136
; Publication No. US20030021770A1
; GENERAL INFORMATION:
; APPLICANT: SCHLOM, JEFFREY
; APPLICANT: KANTOR, JUDITH
; APPLICANT: KUFU, DONALD
; APPLICANT: PANICALI, DENNIS
; APPLICANT: GRITZ, LINDA
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1
; TITLE OF INVENTION: TUMOR-ASSOCIATED ANTIGEN
; FILE REFERENCE: 700953/47113C
; CURRENT APPLICATION NUMBER: US/10/057,136
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 09/366,670
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: PCT/US98/03693
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 60/038,253
; PRIOR FILING DATE: 1997-02-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-057-136-6

Alignment Scores:
Pred. No.: 3.04e-07 Length: 60
Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
```

Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 14 Gaps: 0

US-10-057-136-1 (1-20) x US-10-057-136-6 (1-60)

QY 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
|||||  
DB 1 GGTCAACAGCTCTCCCGCTCATGGGTTACTTGTCTCCAGATACTCGCCCGACTCCA 60

## RESULT 5

US-10-057-136-7

; Sequence 7, Application US/10057136

; Publication No. US20030021770A1

; GENERAL INFORMATION:

; APPLICANT: SCHLOM, JEFFREY

; APPLICANT: KANTOR, JUDITH

; APPLICANT: KUFE, DONALD

; APPLICANT: PANICALI, DENNIS

; APPLICANT: GRITZ, LINDA

; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1

; FILE REFERENCE: 700953/47113C

; CURRENT APPLICATION NUMBER: US/10/057,136

; CURRENT FILING DATE: 2002-01-25

; PRIOR APPLICATION NUMBER: 09/366,670

; PRIOR FILING DATE: 1999-08-03

; PRIOR APPLICATION NUMBER: PCT/US98/03693

; PRIOR FILING DATE: 1998-02-24

; PRIOR APPLICATION NUMBER: 60/038,253

; PRIOR FILING DATE: 1997-02-24

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 7

; LENGTH: 60

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-057-136-7

## Alignment Scores:

Pred. No.: 3.04e-07 Length: 60  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 14 Gaps: 0

US-10-057-136-1 (1-20) x US-10-057-136-7 (1-60)

QY 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
|||||  
DB 1 GGTTCGACGGCCCCCTGCTACGGTGTACATCCGCCCGGATACCGACCGGCCCT 60

## RESULT 6

US-10-057-136-8

; Sequence 8, Application US/10057136

; Publication No. US20030021770A1

; GENERAL INFORMATION:

; APPLICANT: SCHLOM, JEFFREY

; APPLICANT: KANTOR, JUDITH

; APPLICANT: KUFE, DONALD

; APPLICANT: PANICALI, DENNIS

; APPLICANT: GRITZ, LINDA

; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1

; FILE REFERENCE: 700953/47113C

; CURRENT APPLICATION NUMBER: US/10/057,136

; CURRENT FILING DATE: 2002-01-25

; PRIOR APPLICATION NUMBER: 09/366,670

; PRIOR FILING DATE: 1999-08-03

; PRIOR APPLICATION NUMBER: PCT/US98/03693

; PRIOR FILING DATE: 1998-02-24

; PRIOR APPLICATION NUMBER: 60/038,253

; PRIOR FILING DATE: 1997-02-24

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 8

; LENGTH: 60

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-057-136-8

## Alignment Scores:

Pred. No.: 3.04e-07 Length: 60  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 14 Gaps: 0

US-10-057-136-1 (1-20) x US-10-057-136-8 (1-60)

QY 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
|||||  
DB 1 GGCAGCACCGCACCGCCCGCACACGGGGTCAACAAGCGCGCCAGACACTCGACCTGGCGCA 60

## RESULT 7

US-10-057-136-9

; Sequence 9, Application US/10057136

; Publication No. US20030021770A1

; GENERAL INFORMATION:

; APPLICANT: SCHLOM, JEFFREY

; APPLICANT: KANTOR, JUDITH

; APPLICANT: KUFE, DONALD

; APPLICANT: PANICALI, DENNIS

; APPLICANT: GRITZ, LINDA

; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1

; FILE REFERENCE: 700953/47113C

; CURRENT APPLICATION NUMBER: US/10/057,136

; CURRENT FILING DATE: 2002-01-25

; PRIOR APPLICATION NUMBER: 09/366,670

; PRIOR FILING DATE: 1999-08-03

; PRIOR APPLICATION NUMBER: PCT/US98/03693

; PRIOR FILING DATE: 1998-02-24

; PRIOR APPLICATION NUMBER: 60/038,253

; PRIOR FILING DATE: 1997-02-24

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 9

; LENGTH: 60

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-057-136-9

## Alignment Scores:

Pred. No.: 3.04e-07 Length: 60  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 14 Gaps: 0

US-10-057-136-1 (1-20) x US-10-057-136-9 (1-60)

QY 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
|||||  
DB 1 GGAAGTACCGCTCCACTGCACACGGGGTCAACAAGCGCGCCAGACACTCGACCTGGCGCA 60

## RESULT 8

US-10-057-136-10

; Sequence 10, Application US/10057136

; Publication No. US20030021770A1

; GENERAL INFORMATION:

; APPLICANT: SCHLOM, JEFFREY

; APPLICANT: KANTOR, JUDITH

```
; APPLICANT: KUFU, DONALD
; APPLICANT: PANICALI, DENNIS
; APPLICANT: GRITZ, LINDA
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1
; TITLE OF INVENTION: TUMOR-ASSOCIATED ANTIGEN
; FILE REFERENCE: 700953/47113C
; CURRENT APPLICATION NUMBER: US/10/057,136
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 09/366,670
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: PCT/US98/03693
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 60/038,253
; PRIOR FILING DATE: 1997-02-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-057-136-10

Alignment Scores:
Pred. No.: 3.04e-07 Length: 60
Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-057-136-1 (1-20) x US-10-057-136-10 (1-60)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db 1 GGGTCGACTGCCCTCCGGCGCATGGTGTGACCTCAGCTCCTGACACACAAGGCCAGCCCCA 60

RESULT 9
US-10-057-136-11
; Sequence 11, Application US/10057136
; Publication No. US20030021770A1
; GENERAL INFORMATION:
; APPLICANT: SCHLOM, JEFFREY
; APPLICANT: KUFU, DONALD
; APPLICANT: PANICALI, DENNIS
; APPLICANT: GRITZ, LINDA
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1
; TITLE OF INVENTION: TUMOR-ASSOCIATED ANTIGEN
; FILE REFERENCE: 700953/47113C
; CURRENT APPLICATION NUMBER: US/10/057,136
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 09/366,670
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: PCT/US98/03693
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 60/038,253
; PRIOR FILING DATE: 1997-02-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-057-136-11

Alignment Scores:
Pred. No.: 3.04e-07 Length: 60
Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0
```

```
US-10-057-136-1 (1-20) x US-10-057-136-11 (1-60)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db 1 GGTTCACGGCACCTCCAGCACACGGAGTCACGTCCTGCACCCGACACCCGTCAGCTCCG 60

RESULT 10
US-10-057-136-12
; Sequence 12, Application US/10057136
; Publication No. US20030021770A1
; GENERAL INFORMATION:
; APPLICANT: SCHLOM, JEFFREY
; APPLICANT: KANTOR, JUDITH
; APPLICANT: KUFU, DONALD
; APPLICANT: PANICALI, DENNIS
; APPLICANT: GRITZ, LINDA
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1
; TITLE OF INVENTION: TUMOR-ASSOCIATED ANTIGEN
; FILE REFERENCE: 700953/47113C
; CURRENT APPLICATION NUMBER: US/10/057,136
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 09/366,670
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: PCT/US98/03693
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 60/038,253
; PRIOR FILING DATE: 1997-02-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-057-136-12

Alignment Scores:
Pred. No.: 3.04e-07 Length: 60
Score: 109.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-10-057-136-1 (1-20) x US-10-057-136-12 (1-60)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db 1 GGTAGTACAGCGCCACCCGCACATGGCGTCACGAGCGCTCCGGATACGAGACCGGGCGCT 60

RESULT 11
US-10-635-211-3
; Sequence 3, Application US/10635211
; Publication No. US20050031649A1
; GENERAL INFORMATION:
; APPLICANT: Beijing HYDVAX Biotechnology Co. Ltd
; TITLE OF INVENTION: A recombinant fusion protein comprising BCG heat shock protein 65
; TITLE OF INVENTION: and the epitope of MUC1
; FILE REFERENCE: FP03012US
; CURRENT APPLICATION NUMBER: US/10/635,211
; CURRENT FILING DATE: 2003-08-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 120
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(120)
US-10-635-211-3

Alignment Scores:
Pred. No.: 5.69e-07 Length: 120
```

Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 21 Gaps: 0

US-10-057-136-1 (1-20) x US-10-635-211-3 (1-120)

QY 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
|||||  
Db 1 GGTTCTACCGCTCCGCGGCTCACGGTGTACCTTGCTCCGGACACCCGTCGGCTCCG 60

RESULT 12

US-10-635-211-8/c  
; Sequence 8, Application US/10635211  
; Publication No. US20050031649A1  
; GENERAL INFORMATION:

; APPLICANT: Beijing HYDVAX Biotechnology Co. Ltd  
; TITLE OF INVENTION: A recombinant fusion protein comprising BCG heat shock protein 65  
; TITLE OF INVENTION: and the epitope of MUC1  
; FILE REFERENCE: FP03012US  
; CURRENT APPLICATION NUMBER: US/10/635,211  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 8

; LENGTH: 162  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer

US-10-635-211-8

Alignment Scores:

Pred. No.: 7 46e-07 Length: 162  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 21 Gaps: 0

US-10-057-136-1 (1-20) x US-10-635-211-8 (1-162)

QY 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
|||||  
Db 138 GGTTCTACCGCTCCGCGGCTCACGGTGTACCTTGCTCCGGACACCCGTCGGCTCCG 79

RESULT 13

US-10-447-839A-75/c  
; Sequence 75, Application US/10447839A  
; Publication No. US20040018181A1  
; GENERAL INFORMATION:

; APPLICANT: Kufe, Donald W.  
; APPLICANT: Kharbanda, Surender  
; APPLICANT: Weitman, Steven D.

; TITLE OF INVENTION: MUC1 INTERFERENCE RNA COMPOSITIONS AND METHODS DERIVED THEREFROM  
; FILE REFERENCE: 1000.05.009

; CURRENT APPLICATION NUMBER: US/10/447,839A

; PRIOR FILING DATE: 2003-05-29

; PRIOR APPLICATION NUMBER: 10/293,391

; PRIOR FILING DATE: 2002-11-13

; PRIOR APPLICATION NUMBER: 09/951,938

; PRIOR FILING DATE: 2001-09-11

; PRIOR APPLICATION NUMBER: 60/231,841

; PRIOR FILING DATE: 2000-09-11

; NUMBER OF SEQ ID NOS: 109

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 75

; LENGTH: 1424

; TYPE: RNA

; ORGANISM: ARTIFICIAL

; FEATURE:

; OTHER INFORMATION: Synthesized Sequence

US-10-447-839A-75

Alignment Scores:

Pred. No.: 5 35e-06 Length: 1424  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 17 Gaps: 0

US-10-057-136-1 (1-20) x US-10-447-839A-75 (1-1424)

QY 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
|||||  
Db 1041 GGCTCCACCGCCCCCAGCCACGGTGTACCTCGGCCCCGACACACGAGCGGCCCCG 982

RESULT 14

US-10-778-859-75/c

; Sequence 75, Application US/10778859  
; Publication No. US20050042209A1  
; GENERAL INFORMATION:

; APPLICANT: Kufe, Donald W.

; APPLICANT: Ohno, Tsuneya

; TITLE OF INVENTION: MUC1 EXTRACELLULAR DOMAIN AND CANCER TREATMENT COMPOSITIONS AND METHODS DERIVED THEREFROM  
; TITLE OF INVENTION: METHODS DERIVED THEREFROM  
; FILE REFERENCE: 1000.05.011

; CURRENT APPLICATION NUMBER: US/10/778,859

; CURRENT FILING DATE: 2004-02-13

; PRIOR APPLICATION NUMBER: 10/293,391

; PRIOR FILING DATE: 2002-11-13

; PRIOR APPLICATION NUMBER: 10/447,839

; PRIOR FILING DATE: 2003-05-29

; PRIOR APPLICATION NUMBER: 09/951,938

; PRIOR FILING DATE: 2001-09-11

; PRIOR APPLICATION NUMBER: 60/231,841

; PRIOR FILING DATE: 2000-09-11

; NUMBER OF SEQ ID NOS: 111

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 75

; LENGTH: 1424

; TYPE: RNA

; ORGANISM: ARTIFICIAL

; FEATURE:

; OTHER INFORMATION: Synthesized Sequence

US-10-778-859-75

Alignment Scores:

Pred. No.: 5 35e-06 Length: 1424  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 21 Gaps: 0

US-10-057-136-1 (1-20) x US-10-778-859-75 (1-1424)

QY 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
|||||  
Db 1041 GGCTCCACCGCCCCCAGCCACGGTGTACCTCGGCCCCGACACACGAGCGGCCCCG 982

RESULT 15

US-10-447-839A-20

; Sequence 20, Application US/10447839A

; Publication No. US20040018181A1

; GENERAL INFORMATION:

; APPLICANT: Kufe, Donald W.

; APPLICANT: Kharbanda, Surender

; APPLICANT: Weitman, Steven D.

; TITLE OF INVENTION: MUC1 INTERFERENCE RNA COMPOSITIONS AND METHODS DERIVED THEREFROM  
; FILE REFERENCE: 1000.05.009

; CURRENT APPLICATION NUMBER: US/10/447,839A

; CURRENT FILING DATE: 2003-05-29

; PRIOR APPLICATION NUMBER: 10/293,391

; PRIOR FILING DATE: 2002-11-13  
 ; PRIOR APPLICATION NUMBER: 09/951,938  
 ; PRIOR FILING DATE: 2001-09-11  
 ; PRIOR APPLICATION NUMBER: 60/231,841  
 ; PRIOR FILING DATE: 2000-09-11  
 ; NUMBER OF SEQ ID NOS: 109  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 20  
 ; LENGTH: 1428  
 ; TYPE: RNA  
 ; ORGANISM: RNA  
 US-10-447-839A-20

Alignment Scores:  
 Pred. No.: 5.36e-06 Length: 1428  
 Score: 109.00 Matches: 20  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 17 Gaps: 0

US-10-057-136-1 (1-20) x US-10-447-839A-20 (1-1428)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
 Db 385 GGCUCACCCGCCCCAGCCACGGUGUACCCGCCGACACCCAGCGGCCCG 444

Search completed: June 30, 2005, 09:12:19  
 Job time : 1601 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 30, 2005, 07:12:04 ; Search time 131 Seconds  
(without alignments)  
249.813 Million cell updates/sec

Title: US-10-057-136-1  
Perfect score: 109  
Sequence: 1 GSTAPPAHGVTSPDTRPAP 20  
Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0  
Searched: 1202784.seqs, 818138359 residues  
Total number of hits satisfying chosen parameters: 2405568  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Command line parameters:  
-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/cgn2\_1/USPTO spool/US10057136/runat 29062005 162123 11409/app query.fasta\_1.199  
-DB=Issued\_Patents\_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10057136 @CGN\_1 1 69 @runat 29062005 162123 11409 -NCPU=6 -ICPU=3  
-NO MMAP -LARGESQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued\_Patents\_NA:  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/pctus\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query		DB ID	Description
	Score	Match Length		
1	109	100.0	1804	4 US-10-029-517-17 Sequence 17, Appl
2	109	100.0	8186	4 US-10-029-517-19 Sequence 19, Appl
3	104	95.4	1721	4 US-10-029-517-3 Sequence 3, Appl
4	102	93.6	518	4 US-10-029-517-101 Sequence 101, Appl
5	101	92.7	572	4 US-10-029-517-18 Sequence 18, Appl
6	98	89.9	60	4 US-09-475-947A-246 Sequence 246, Appl
7	97	89.0	981	4 US-10-029-517-16 Sequence 16, Appl
8	97	89.0	3343	4 US-10-029-517-102 Sequence 102, Appl
9	95	87.2	519	4 US-09-646-028-42 Sequence 42, Appl
10	95	87.2	534	4 US-09-646-028-46 Sequence 46, Appl
11	91	83.5	6192	2 US-08-479-537A-1 Sequence 1, Appli
12	91	83.5	6192	3 US-09-083-116-1 Sequence 1, Appli

13	91	83.5	6192	3	US-09-134-916A-1	Sequence 1, Appli
14	91	83.5	6449	2	US-08-479-537A-4	Sequence 4, Appli
15	91	83.5	6449	3	US-09-083-116-4	Sequence 4, Appli
16	91	83.5	6449	3	US-09-134-916A-4	Sequence 4, Appli
c 17	61	56.0	819	4	US-09-902-540-5683	Sequence 5683, Ap
c 18	61	56.0	50725	4	US-09-902-540-1271	Sequence 1271, Ap
19	59	54.1	954	3	US-08-680-506-5	Sequence 5, Appli
20	59	54.1	1347	3	US-08-680-506-8	Sequence 8, Appli
21	59	54.1	1587	3	US-08-680-506-6	Sequence 6, Appli
22	59	54.1	2233	3	US-08-680-506-4	Sequence 4, Appli
23	59	54.1	5027	3	US-08-680-506-2	Sequence 2, Appli
c 24	58	53.2	119981	4	US-09-949-016-11844	Sequence 11844, A
c 25	58	53.2	119982	4	US-09-949-016-13606	Sequence 13606, A
c 26	57.5	52.8	3333	4	US-09-902-540-4753	Sequence 4753, Ap
27	57.5	52.8	14809	4	US-09-902-540-1032	Sequence 1032, Ap
c 28	57.5	52.8	33529	3	US-09-144-085-3	Sequence 3, Appli
29	56	51.4	9653	4	US-09-949-016-12275	Sequence 12275, A
30	56	51.4	9653	4	US-09-949-016-13090	Sequence 13090, A
c 31	56	51.4	16427	4	US-09-902-540-1160	Sequence 1160, Ap
32	55.5	50.9	3453	4	US-10-101-464A-861	Sequence 861, App
33	55	50.5	714	4	US-09-252-991A-907	Sequence 907, App
c 34	55	50.5	1362	4	US-09-489-039A-3117	Sequence 3117, Ap
c 35	55	50.5	1551	4	US-09-252-991A-1128	Sequence 1128, Ap
36	55	50.5	2115	4	US-09-252-991A-952	Sequence 952, App
37	55	50.5	18159	4	US-09-949-016-12401	Sequence 12401, A
38	55	50.5	18160	4	US-09-949-016-13677	Sequence 13677, A
c 39	54.5	50.0	41768	4	US-09-902-540-1266	Sequence 1266, Ap
c 40	54.5	50.0	44479	4	US-09-949-016-17176	Sequence 17176, A
41	54	49.5	407	4	US-09-513-999C-2147	Sequence 2147, Ap
42	54	49.5	603	4	US-09-902-540-8033	Sequence 8033, Ap
43	54	49.5	762	4	US-09-252-991A-11986	Sequence 11986, A
44	54	49.5	1125	4	US-09-252-991A-11956	Sequence 11956, A
45	54	49.5	2073	4	US-09-902-540-5730	Sequence 5730, Ap

ALIGNMENTS

RESULT 1

US-10-029-517-17  
; Sequence 17, Application US/10029517  
; Patent No. 6716627  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth W. Dobie  
; APPLICANT: Susan J. Myers  
; TITLE OF INVENTION: ANTISENSE MODULATION OF MUCIN 1, TRANSMEMBRANE EXPRESSION  
; FILE REFERENCE: RTS-0352  
; CURRENT APPLICATION NUMBER: US/10/029,517  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 107  
; SEQ ID NO 17  
; LENGTH: 1804  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (73)...(1500)  
US-10-029-517-17

Alignment Scores:  
Pred. No.: 2.86e-05 Length: 1804  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-057-136-1 (1-20) x US-10-029-517-17 (1-1804)

Qy 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
|||||  
Db 457 GGCTCCACCCGCCCGCCAGCCACGGTGTCACCTCGGCCCGGACACCGCGGCCCG 516

RESULT 2

US-10-029-517-19  
; Sequence 19, Application US/10029517  
; Patent No. 6716627  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth W. Dobie  
; APPLICANT: Susan J. Myers  
; TITLE OF INVENTION: ANTISENSE MODULATION OF MUCIN 1, TRANSMEMBRANE EXPRESSION  
; FILE REFERENCE: RTS-0352  
; CURRENT APPLICATION NUMBER: US/10/029,517  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 107  
; SEQ ID NO 19  
; LENGTH: 8186  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: 6899  
; OTHER INFORMATION: unknown  
; NAME/KEY: unsure  
; LOCATION: 7155  
; OTHER INFORMATION: unknown  
; NAME/KEY: unsure  
; LOCATION: 7184  
; OTHER INFORMATION: unknown  
; NAME/KEY: unsure  
; LOCATION: 7957  
; OTHER INFORMATION: unknown  
; NAME/KEY: intron  
; LOCATION: (2997)...(3498)  
; OTHER INFORMATION: intron 1  
; NAME/KEY: intron:exon junction  
; LOCATION: (3498)...(3499)  
; OTHER INFORMATION: intron 1:exon 2  
; NAME/KEY: exon  
; LOCATION: (3508)...(3599)  
; OTHER INFORMATION: exon 2d  
; NAME/KEY: exon:intron junction  
; LOCATION: (3982)...(3983)  
; OTHER INFORMATION: exon 2a:intron 2a  
; NAME/KEY: intron:exon junction  
; LOCATION: (4205)...(4206)  
; OTHER INFORMATION: intron 2c:exon 3c  
; NAME/KEY: intron:exon junction  
; LOCATION: (4259)...(4260)  
; OTHER INFORMATION: intron 2d:exon 3d  
; NAME/KEY: exon  
; LOCATION: (4260)...(4328)  
; OTHER INFORMATION: exon 3d  
; NAME/KEY: intron:exon junction  
; LOCATION: (4632)...(4633)  
; OTHER INFORMATION: intron 3:exon 4  
; NAME/KEY: exon  
; LOCATION: (4914)...(5035)  
; OTHER INFORMATION: exon 5  
; NAME/KEY: intron  
; LOCATION: (5266)...(6293)  
; OTHER INFORMATION: intron 6  
US-10-029-517-19

Alignment Scores:  
Pred. No.: 0.000151 Length: 8186  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-10-057-136-1 (1-20) x US-10-029-517-19 (1-8186)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
|||  
Db 3825 GGCTCCACCGCCCCCGCCAGCCCGGTGTACCTCGGCCCGGACACCGAGCGGCCCG 3884

## RESULT 3

US-10-029-517-3  
; Sequence 3, Application US/10029517  
; Patent No. 6716627  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth W. Dobie  
; APPLICANT: Susan J. Myers  
; TITLE OF INVENTION: ANTISENSE MODULATION OF MUCIN 1, TRANSMEMBRANE EXPRESSION  
; FILE REFERENCE: RTS-0352  
; CURRENT APPLICATION NUMBER: US/10/029,517  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 107  
; SEQ ID NO 3  
; LENGTH: 1721  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (58)...(1605)  
US-10-029-517-3

## Alignment Scores:

Pred. No.: 0.000122 Length: 1721  
Score: 104.00 Matches: 19  
Percent Similarity: 95.00% Conservative: 0  
Best Local Similarity: 95.00% Mismatches: 1  
Query Match: 95.41% Indels: 0  
DB: 4 Gaps: 0

US-10-057-136-1 (1-20) x US-10-029-517-3 (1-1721)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
|||  
Db 442 GGCTCCACCGCCCCCGCCAGCCCGGTGTACCTCGGCCCGGACACCGAGCGGCCCG 501

## RESULT 4

US-10-029-517-101  
; Sequence 101, Application US/10029517  
; Patent No. 6716627  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth W. Dobie  
; APPLICANT: Susan J. Myers  
; TITLE OF INVENTION: ANTISENSE MODULATION OF MUCIN 1, TRANSMEMBRANE EXPRESSION  
; FILE REFERENCE: RTS-0352  
; CURRENT APPLICATION NUMBER: US/10/029,517  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 107  
; SEQ ID NO 101  
; LENGTH: 518  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
US-10-029-517-101

## Alignment Scores:

Pred. No.: 5.95e-05 Length: 518  
Score: 102.00 Matches: 19  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 93.58% Indels: 0  
DB: 4 Gaps: 0

US-10-057-136-1 (1-20) x US-10-029-517-101 (1-518)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAla 19  
|||  
Db 462 GGCTCCACCGCCCCCGCCAGCCCGGTGTACCTCGGCCCGGACACCGAGCGGCCCG 518

## RESULT 5

US-10-029-517-18  
; Sequence 18, Application US/10029517  
; Patent No. 6716627

```

; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Susan J. Myers
; TITLE OF INVENTION: ANTISENSE MODULATION OF MUCIN 1, TRANSMEMBRANE EXPRESSION
; FILE REFERENCE: RTS-0352
; CURRENT APPLICATION NUMBER: US/10/029,517
; CURRENT FILING DATE: 2001-12-20
; SEQ ID NO 18
; LENGTH: 572
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (67)...(572)
US-10-029-517-18

Alignment Scores:
Pred. No.: 8.97e-05 Length: 572
Score: 101.00 Matches: 19
Percent Similarity: 95.00% Conservatives: 0
Best Local Similarity: 95.00% Mismatches: 1
Query Match: 92.66% Indels: 0
DB: 4 Gaps: 0

US-10-057-136-1 (1-20) x US-10-029-517-18 (1-572)

Qy 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db 478 GGCTCCACCGCCCGCCCAAGCCACCGGTGTACCTCGGCCCGGACACACCGGCCCG 537

RESULT 6
US-09-475-947A-246
; Sequence 246, Application US/09475947A
; Patent No. 6472154
; GENERAL INFORMATION:
; APPLICANT: Garner, Harold R.
; APPLICANT: Wren, Jonathan D.
; APPLICANT: Minna, John D.
; TITLE OF INVENTION: Polymorphic Repeats in Human Genes
; FILE REFERENCE: UTSD0667
; CURRENT APPLICATION NUMBER: US/09/475,947A
; CURRENT FILING DATE: 1999-12-31
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 246
; LENGTH: 60
; TYPE: DNA
; ORGANISM: human
US-09-475-947A-246

Alignment Scores:
Pred. No.: 1.85e-05 Length: 60
Score: 98.00 Matches: 18
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 89.91% Indels: 0
DB: 4 Gaps: 0

US-10-057-136-1 (1-20) x US-09-475-947A-246 (1-60)

Qy 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgPro 18
Db 7 GGCTCCACCGCCCGCCCAAGCCACCGGTGTACCTCGGCCCGGACACACCGGCCCG 60

RESULT 7
US-10-029-517-16
; Sequence 16, Application US/10029517
; Patent No. 6716627
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Susan J. Myers
; TITLE OF INVENTION: ANTISENSE MODULATION OF MUCIN 1, TRANSMEMBRANE EXPRESSION

```

```

; FILE REFERENCE: RTS-0352
; CURRENT APPLICATION NUMBER: US/10/029,517
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 107
; SEQ ID NO 16
; LENGTH: 981
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon:exon junction
; LOCATION: (464)...(465)
; OTHER INFORMATION: exon 3b:exon 4
US-10-029-517-16

Alignment Scores:
Pred. No.: 0.000541 Length: 981
Score: 97.00 Matches: 18
Percent Similarity: 94.74% Conservatives: 0
Best Local Similarity: 94.74% Mismatches: 1
Query Match: 88.99% Indels: 0
DB: 4 Gaps: 0

US-10-057-136-1 (1-20) x US-10-029-517-16 (1-981)

Qy 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAla 19
Db 21 GGCTCCACCGCCCGCCCAAGCCACCGGTGTACCTCGGCCCGGACACACCGGCCCG 77

RESULT 8
US-10-029-517-102
; Sequence 102, Application US/10029517
; Patent No. 6716627
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; APPLICANT: Susan J. Myers
; TITLE OF INVENTION: ANTISENSE MODULATION OF MUCIN 1, TRANSMEMBRANE EXPRESSION
; FILE REFERENCE: RTS-0352
; CURRENT APPLICATION NUMBER: US/10/029,517
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 107
; SEQ ID NO 102
; LENGTH: 3343
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-10-029-517-102

Alignment Scores:
Pred. No.: 0.00208 Length: 3343
Score: 97.00 Matches: 18
Percent Similarity: 94.74% Conservatives: 0
Best Local Similarity: 94.74% Mismatches: 1
Query Match: 88.99% Indels: 0
DB: 4 Gaps: 0

US-10-057-136-1 (1-20) x US-10-029-517-102 (1-3343)

Qy 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAla 19
Db 1728 GGCTCCACCGCCCGCCCAAGCCACCGGTGTACCTCGGCCCGGACACACCGGCCCG 1784

RESULT 9
US-09-646-028-42
; Sequence 42, Application US/09646028
; Patent No. 6562347
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Biragyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/09/646,028
; CURRENT FILING DATE: 2000-09-12

```

```

; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 519
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-42

Alignment Scores:
Pred. No.:      0.00049      Length:      519
Score:          95.00      Matches:      20
Percent Similarity: 71.43%      Conservative: 0
Best Local Similarity: 71.43%      Mismatches: 0
Query Match:      87.16%      Indels:      8
DB:              4              Gaps:      1

US-10-057-136-1 (1-20) x US-09-646-028-42 (1-519)

QY      1 GlySerThrAlaProProAlaHis-----GlyValThrSer 12
      |||
Db      331 GGTTCCTACTGCTCGCGCGCACACGGGTGTAACCTCTGCCGCCCTCGACGGTGTAACTTCT 390
      |||

QY      13 AlaProAspThrArgProAlaPro 20
      |||
Db      391 GCCCGGACACTCGCCCGACACCG 414

RESULT 10
US-09-646-028-46
; Sequence 46, Application US/09646028
; Patent No. 6562347
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Biragyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/09/646,028
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 46
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-46

Alignment Scores:
Pred. No.:      0.000506      Length:      534
Score:          95.00      Matches:      20
Percent Similarity: 71.43%      Conservative: 0
Best Local Similarity: 71.43%      Mismatches: 0
Query Match:      87.16%      Indels:      8
DB:              4              Gaps:      1

US-10-057-136-1 (1-20) x US-09-646-028-46 (1-534)

QY      1 GlySerThrAlaProProAlaHis-----GlyValThrSer 12
      |||
Db      346 GGTTCCTACTGCTCGCGCGCACACGGGTGTAACCTCTGCCGCCCTCGACGGTGTAACTTCT 405
      |||

QY      13 AlaProAspThrArgProAlaPro 20
      |||
Db      406 GCCCGGACACTCGCCCGACACCG 429

RESULT 11
```

```

US-08-479-537A-1
; Sequence 1, Application US/08479537A
; Patent No. 5861381
; GENERAL INFORMATION:
; APPLICANT: CHAMBON, Pierre
; APPLICANT: KIENY, Marie-Paule
; APPLICANT: LATHE, Richard
; APPLICANT: HAREUVENI, Mara
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE
; TITLE OF INVENTION: TREATMENT OR PREVENTION OF A MALIGNANT TUMOR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,537A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 90/13101
; FILING DATE: 23-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR91/00835
; FILING DATE: 23-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,320
; FILING DATE: 04-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,576
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 017753-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6192 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 58..120
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 439..5239
; OTHER INFORMATION: /note="The nucleotides spanning
; OTHER INFORMATION: 439-5239 constitute a repeated region wherein the repeat is 6
; OTHER INFORMATION: nucleotides and encodes 20 amino acids, 17 of which are fixed
; OTHER INFORMATION: The number of such repeats varies from 1 to 80."
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 121..6166
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 457
; OTHER INFORMATION: /note="Nucleotide 457 is X1 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
; FEATURE:
```

```

; NAME/KEY: repeat_region
; LOCATION: 487
; OTHER INFORMATION: /note= "Nucleotide 487 is Y = NNN
; OTHER INFORMATION: which is the codon for Thr or Asn wherein Thr = ACT, ACC, ACA
; OTHER INFORMATION: or ACG; and Asn = AAT or AAC."
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 496
; OTHER INFORMATION: /note= "Nucleotide 496 is X2 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
US-08-479-537A-1

Alignment Scores:
Pred. No.: 0.0249 Length: 6192
Score: 91.00 Matches: 17
Percent Similarity: 85.00% Conservative: 0
Best Local Similarity: 85.00% Mismatches: 3
Query Match: 83.49% Indels: 0
DB: 2 Gaps: 0

US-10-057-136-1 (1-20) x US-08-479-537A-1 (1-6192)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
|||||
Db 442 GGCTCCACCGCCCNNGCCACCGGTGTACCTCGGCCCGGACNNAGGCCGNNCCG 501

RESULT 12
US-09-083-116-1
; Sequence 1, Application US/09083116
; Patent No. 6203795
; GENERAL INFORMATION:
; APPLICANT: CHAMBER, Pierre
; APPLICANT: KIENY, Marie-Paule
; APPLICANT: LATHE, Richard
; APPLICANT: HAREUVENI, Mara
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE
; TITLE OF INVENTION: TREATMENT OR PREVENTION OF A MALIGNANT TUMOR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/083.116
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/479,537
; FILING DATE:
; APPLICATION NUMBER: WO PCT/FR91/00835
; FILING DATE: 23-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,320
; FILING DATE: 04-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,576
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 017753-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620

```

```

; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6192 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 58..120
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 439..5239
; OTHER INFORMATION: /note= "The nucleotides spanning
; OTHER INFORMATION: 439-5239 constitute a repeated region wherein the repeat is 6
; OTHER INFORMATION: nucleotides and encodes 20 amino acids, 17 of which are fixed
; OTHER INFORMATION: The number of such repeats varies from 1 to 80."
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 121..6166
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 457
; OTHER INFORMATION: /note= "Nucleotide 457 is X1 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 487
; OTHER INFORMATION: /note= "Nucleotide 487 is Y = NNN
; OTHER INFORMATION: which is the codon for Thr or Asn wherein Thr = ACT, ACC, ACA
; OTHER INFORMATION: or ACG; and Asn = AAT or AAC."
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 496
; OTHER INFORMATION: /note= "Nucleotide 496 is X2 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
US-09-083-116-1

Alignment Scores:
Pred. No.: 0.0249 Length: 6192
Score: 91.00 Matches: 17
Percent Similarity: 85.00% Conservative: 0
Best Local Similarity: 85.00% Mismatches: 3
Query Match: 83.49% Indels: 0
DB: 3 Gaps: 0

US-10-057-136-1 (1-20) x US-09-083-116-1 (1-6192)

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
|||||
Db 442 GGCTCCACCGCCCNNGCCACCGGTGTACCTCGGCCCGGACNNAGGCCGNNCCG 501

RESULT 13
US-09-134-916A-1
; Sequence 1, Application US/09134916A
; Patent No. 6328956
; GENERAL INFORMATION:
; APPLICANT: CHAMBER, Pierre
; APPLICANT: KIENY, Marie-Paule
; APPLICANT: LATHE, Richard
; APPLICANT: HAREUVENI, Mara
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE
; TITLE OF INVENTION: TREATMENT OR PREVENTION OF A MALIGNANT TUMOR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States

```

```

; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,916A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: US/08/479,537
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: FR 90/13101
; FILING DATE: 23-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR91/00835
; FILING DATE: 23-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,320
; FILING DATE: 04-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,576
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 017753-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6192 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 58..120
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 439..5239
; OTHER INFORMATION: /note= "The nucleotides spanning
; OTHER INFORMATION: 439-5239 constitute a repeated region wherein the repeat is 6
; OTHER INFORMATION: nucleotides and encodes 20 amino acids, 17 of which are fixed
; OTHER INFORMATION: The number of such repeats varies from 1 to 80."
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 121..6166
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 457
; OTHER INFORMATION: /note= "Nucleotide 457 is X1 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 487
; OTHER INFORMATION: /note= "Nucleotide 487 is Y = NNN
; OTHER INFORMATION: which is the codon for Thr or Asn wherein Thr = ACT, ACC, ACA
; OTHER INFORMATION: or ACG; and Asn = AAT or AAC."
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 496
; OTHER INFORMATION: /note= "Nucleotide 496 is X2 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
; US-09-134-916A-1
;
Alignment Scores:
Pred. No.: 0.0249 Length: 6192

```

```

Score: 91.00 Matches: 17
Percent Similarity: 85.00% Conservative: 0
Best Local Similarity: 85.00% Mismatches: 3
Query Match: 83.49% Indels: 0
DB: 3 Gaps: 0

US-10-057-136-1 (1-20) x US-09-134-916A-1 (1-6192)

QY 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
   |||||
Db 442 GGCTCCACCGCCCCNNNGCCACCGGTGTACCTCGGCCCGGACNNNAGCCGNNCCG 501
   |||||

RESULT 14
US-08-479-537A-4
; Sequence 4, Application US/08479537A
; Patent No. 5861381
; GENERAL INFORMATION:
; APPLICANT: CHAMBER, Pierre
; APPLICANT: KIENY, Marie-Paule
; APPLICANT: LATHE, Richard
; APPLICANT: HAREUVENI, Mara
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE
; TREATMENT OR PREVENTION OF A MALIGNANT TUMOR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,537A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 90/13101
; FILING DATE: 23-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR91/00835
; FILING DATE: 23-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,320
; FILING DATE: 04-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,576
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 017753-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6449 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 58..120
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 439..5239
; OTHER INFORMATION: /note= "The nucleotides spanning

```



```

; OTHER INFORMATION: 439-5239 constitute a repeated region wherein the repeat is 6
; OTHER INFORMATION: nucleotides and encodes 20 amino acids, 17 of which are fixed
; OTHER INFORMATION: The number of such repeats varies from 1 to 80."
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 121..5661
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 457
; OTHER INFORMATION: /note= "Nucleotide 457 is X1 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 487
; OTHER INFORMATION: /note= "Nucleotide 487 is Y = NNN
; OTHER INFORMATION: which is the codon for Thr or Asn wherein Thr = ACT, ACC, ACA
; OTHER INFORMATION: or ACG; and Asn = AAT or AAC."
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 496
; OTHER INFORMATION: /note= "Nucleotide 496 is X2 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
; US-08-479-537A-4

```

```

Alignment Scores:
Pred. No.: 0.0261 Length: 6449
Score: 91.00 Matches: 17
Percent Similarity: 85.00% Conservative: 0
Best Local Similarity: 85.00% Mismatches: 3
Query Match: 83.49% Indels: 0
DB: 2 Gaps: 0

```

US-10-057-136-1 (1-20) x US-08-479-537A-4 (1-6449)

```

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db 442 GGCTCCACCGCCCNNGCCACCGGTGTACCTCGGCCCGACNNNAGCGGNNCCG 501

```

RESULT 15

```

US-09-083-116-4
; Sequence 4, Application US/09083116
; Patent No. 6203795
; GENERAL INFORMATION:
; APPLICANT: CHAMBER, Pierre
; APPLICANT: KIENY, Marie-Paule
; APPLICANT: LATHE, Richard
; APPLICANT: HAREUVENI, Mara
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR THE
; TREATMENT OR PREVENTION OF A MALIGNANT TUMOR
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/083,116
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/479,537
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/FR91/00835

```

```

; FILING DATE: 23-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/039,320
; FILING DATE: 04-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/403,576
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 017753-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6449 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 58..120
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 439..5239
; OTHER INFORMATION: /note= "The nucleotides spanning
; 439-5239 constitute a repeated region wherein the repeat is 6
; amino acids, 17 of which are fixed
; from 1 to 80."
; OTHER INFORMATION: The number of such repeats varies from 1 to 80."
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 121..5661
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 457
; OTHER INFORMATION: /note= "Nucleotide 457 is X1 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: 496
; OTHER INFORMATION: /note= "Nucleotide 496 is X2 = NNN
; OTHER INFORMATION: which is the codon for Pro or Ala wherein Pro = CCT, CCC, CCA
; OTHER INFORMATION: or CCG; and Ala = GCT, GCC, GCA, or GCG."
; US-09-083-116-4

```

```

Alignment Scores:
Pred. No.: 0.0261 Length: 6449
Score: 91.00 Matches: 17
Percent Similarity: 85.00% Conservative: 0
Best Local Similarity: 85.00% Mismatches: 3
Query Match: 83.49% Indels: 0
DB: 3 Gaps: 0

```

US-10-057-136-1 (1-20) x US-09-083-116-4 (1-6449)

```

Qy 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db 442 GGCTCCACCGCCCNNGCCACCGGTGTACCTCGGCCCGACNNNAGCGGNNCCG 501

```

Search completed: June 30, 2005, 08:45:34  
Job time : 134 secs

**THIS PAGE BLANK (USPTO)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 30, 2005, 06:44:14 ; Search time 359 Seconds  
(without alignments)  
329.791 Million cell updates/sec

Title: US-10-057-136-1

Perfect score: 109

Sequence: 1 GSTAPPAHGVTSPDTRPAP 20

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh  
-Q=/cgn2\_1/USPTO\_spool/US10057136/runat\_29062005\_162122\_11378/app\_query.fasta\_1.199  
-DB=N\_Geneseq\_16Dec04 -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10057136 @CGN\_1\_1\_470 @runat\_29062005\_162122\_11378 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N\_Geneseq\_16Dec04:  
1: Geneseqn1980s:  
2: Geneseqn1990s:  
3: Geneseqn2000s:  
4: Geneseqn2001as:  
5: Geneseqn2001bs:  
6: Geneseqn2002as:  
7: Geneseqn2002bs:  
8: Geneseqn2003as:  
9: Geneseqn2003bs:  
10: Geneseqn2003cs:  
11: Geneseqn2003ds:  
12: Geneseqn2004as:  
13: Geneseqn2004bs:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	109	100.0	60	2 AAV48320	AAV48320 Nucleotid
2	109	100.0	60	2 AAV48321	AAV48321 Nucleotid
3	109	100.0	60	2 AAV48325	AAV48325 Nucleotid
4	109	100.0	60	2 AAV48322	AAV48322 Nucleotid
5	109	100.0	60	2 AAV48324	AAV48324 Nucleotid

6	109	100.0	60	2 AAV48318	AAV48318 Nucleotid
7	109	100.0	60	2 AAV48323	AAV48323 Nucleotid
8	109	100.0	60	2 AAV48316	AAV48316 Nucleotid
9	109	100.0	60	2 AAV48319	AAV48319 Nucleotid
10	109	100.0	60	2 AAV48317	AAV48317 Nucleotid
c 11	109	100.0	156	10 ADK68635	ADK68635 HSP65-MUC
c 12	109	100.0	309	1 AAN90579	AAN90579 pDF9.3 CD
13	109	100.0	525	3 AAD00385	AAD00385 Human Muc
14	109	100.0	891	3 AAD00391	AAD00391 Ubiquitin
15	109	100.0	1194	12 ADI57712	ADI57712 Human bre
16	109	100.0	1371	3 AAD00388	AAD00388 Human Muc
17	109	100.0	1378	12 ADI57693	ADI57693 Human bre
18	109	100.0	1424	12 ADO23180	ADO23180 Antisense
c 19	109	100.0	1428	6 ABL60159	ABL60159 Human MUC
20	109	100.0	1428	12 ADO23125	ADO23125 Human MUC
21	109	100.0	1457	12 ADF32627	ADF32627 Plasmid J
22	109	100.0	1527	2 AAV48329	AAV48329 MiniMUC1
23	109	100.0	1614	12 ADK70370	ADK70370 Respirato
24	109	100.0	1630	12 ADI57708	ADI57708 Human bre
25	109	100.0	1634	12 ADI57689	ADI57689 Human bre
26	109	100.0	1712	12 ADI57686	ADI57686 Human bre
27	109	100.0	1737	3 AAD00394	AAD00394 Ubiquitin
28	109	100.0	1738	12 ADI57669	ADI57669 Human bre
29	109	100.0	1755	12 ADI57673	ADI57673 Human bre
30	109	100.0	1774	12 ADE43991	ADE43991 Plasmid J
31	109	100.0	1774	12 ADF32625	ADF32625 Plasmid J
32	109	100.0	1799	12 ADO23124	ADO23124 Human MUC
33	109	100.0	1800	13 ADR89853	ADR89853 Human muc
34	109	100.0	1803	12 ADI57699	ADI57699 Human bre
35	109	100.0	1804	6 ABL67539	ABL67539 Thyroid c
36	109	100.0	1804	9 AAD56950	AAD56950 Human muc
37	109	100.0	1804	10 ADD14719	ADD14719 Human src
38	109	100.0	1804	12 ADP13294	ADP13294 Renal cel
39	109	100.0	1805	12 ADO28642	ADO28642 Human MUC
40	109	100.0	1805	12 ADQ83917	ADQ83917 Human tum
41	109	100.0	1805	12 ADQ86329	ADQ86329 Human tum
42	109	100.0	1805	12 ADQ85148	ADQ85148 Human tum
43	109	100.0	1805	13 ADQ83237	ADQ83237 Human tum
44	109	100.0	1808	12 ADI57706	ADI57706 Human bre
45	109	100.0	1818	12 ADF32633	ADF32633 Plasmid J

ALIGNMENTS

RESULT 1  
AAV48320  
ID AAV48320 standard; DNA; 60 BP.

XX AAV48320;

AC AAV48320;

XX 20-NOV-1998 (first entry)

XX Nucleotide sequence encoding MUC1 tandem repeat unit R5.

DE ss; MUC1; recombinant pox virus; cytotoxic T-lymphocyte; immunogen;

XX tumour; tumour-associated antigen.

XX Homo sapiens.

XX WO9837095-A2.

XX 27-AUG-1998.

XX 24-FEB-1998; 98WO-US003693.

XX 24-FEB-1997; 97US-0038253P.

XX (THER-) THERION BIOLOGICS CORP.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX (DAND ) DANA FARBER CANCER INST INC.

XX Schlom J, Kantor J, Kufe D, Panicali D, Gritz'L;

DR WPI; 1998-467492/40.

XX New recombinant pox virus for tumour therapy - comprises DNA encoding an

PT immunogenic mini-MUC1 fragment comprising 5-25 MUC1 tandem repeat units.

XX Disclosure; Page 11; 42pp; English.

XX The MUC1 tandem repeat units AAV48317-V48325 were used to create an

CC immunogenic mini-MUC1 fragment for inclusion in a recombinant pox virus

CC (RPV). The RPV was used in a pharmaceutical composition also containing

CC an immunomodulator to generate MUC1 specific cytotoxic T-lymphocytes. The

CC recombinant pox virus therefore encodes an immunogenic MUC1 fragment that

CC does not undergo significant genetic deletion, thereby providing an

CC unexpectedly stable and immunogenic pox virus. They can be used to

CC prevent or treat tumours expressing MUC1 tumour-associated antigens

XX Sequence 60 BP; 9 A; 27 C; 15 G; 9 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.26e-06	Length:	60
Score:	109.00	Matches:	20
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	2	Gaps:	0

US-10-057-136-1 (1-20) x AAV48320 (1-60)

QY 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20

Db 1 GGTTCGACGGCCCCCTGCTCACGGGTGAACATCCGCCCGGATACCGACCGGCCCT 60

RESULT 2

AAV48321

ID AAV48321 standard; DNA; 60 BP.

XX AAV48321;

XX 20-NOV-1998 (first entry)

DT Nucleotide sequence encoding MUC1 tandem repeat unit R6.

DE ss; MUC1; recombinant pox virus; cytotoxic T-lymphocyte; immunogen;

XX tumour; tumour-associated antigen.

OS Homo sapiens.

XX WO9837095-A2.

XX 27-AUG-1998.

PF 24-FEB-1998; 98WO-US003693.

XX 24-FEB-1997; 97US-0038253P.

XX (THER-) THERION BIOLOGICS CORP.

PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PA (DAND ) DANA FARBER CANCER INST INC.

XX Schlom J, Kantor J, Kufe D, Panicali D, Gritz L;

PI WPI; 1998-467492/40.

XX New recombinant pox virus for tumour therapy - comprises DNA encoding an

PT immunogenic mini-MUC1 fragment comprising 5-25 MUC1 tandem repeat units.

XX Disclosure; Page 11; 42pp; English.

XX The MUC1 tandem repeat units AAV48317-V48325 were used to create an

CC immunogenic mini-MUC1 fragment for inclusion in a recombinant pox virus

CC (RPV). The RPV was used in a pharmaceutical composition also containing

CC an immunomodulator to generate MUC1 specific cytotoxic T-lymphocytes. The

CC recombinant pox virus therefore encodes an immunogenic MUC1 fragment that

CC does not undergo significant genetic deletion, thereby providing an

CC unexpectedly stable and immunogenic pox virus. They can be used to

CC prevent or treat tumours expressing MUC1 tumour-associated antigens

XX Sequence 60 BP; 13 A; 27 C; 17 G; 3 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.26e-06	Length:	60
Score:	109.00	Matches:	20
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	2	Gaps:	0

US-10-057-136-1 (1-20) x AAV48321 (1-60)

QY 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20

Db 1 GGCAGCACCGCACCGCCCGCACACGCGGGTCAAGCGCGCCGACACTCGACCTGCGCCA 60

RESULT 3

AAV48325

ID AAV48325 standard; DNA; 60 BP.

XX AAV48325;

XX 20-NOV-1998 (first entry)

DT Nucleotide sequence encoding MUC1 tandem repeat unit R10.

DE ss; MUC1; recombinant pox virus; cytotoxic T-lymphocyte; immunogen;

XX tumour; tumour-associated antigen.

OS Homo sapiens.

XX WO9837095-A2.

XX 27-AUG-1998.

PF 24-FEB-1998; 98WO-US003693.

XX 24-FEB-1997; 97US-0038253P.

XX (THER-) THERION BIOLOGICS CORP.

PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PA (DAND ) DANA FARBER CANCER INST INC.

XX Schlom J, Kantor J, Kufe D, Panicali D, Gritz L;

PI WPI; 1998-467492/40.

XX New recombinant pox virus for tumour therapy - comprises DNA encoding an

PT immunogenic mini-MUC1 fragment comprising 5-25 MUC1 tandem repeat units.

XX Disclosure; Page 11; 42pp; English.

XX The MUC1 tandem repeat units AAV48317-V48325 were used to create an

CC immunogenic mini-MUC1 fragment for inclusion in a recombinant pox virus

CC (RPV). The RPV was used in a pharmaceutical composition also containing

CC an immunomodulator to generate MUC1 specific cytotoxic T-lymphocytes. The

CC recombinant pox virus therefore encodes an immunogenic MUC1 fragment that

CC does not undergo significant genetic deletion, thereby providing an

CC unexpectedly stable and immunogenic pox virus. They can be used to

CC prevent or treat tumours expressing MUC1 tumour-associated antigens

XX Sequence 60 BP; 12 A; 22 C; 19 G; 7 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	6.26e-06	Length:	60
Score:	109.00	Matches:	20
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0



XX PD 27-AUG-1998.  
XX PF 24-FEB-1998; 98WO-US003693.  
XX PR 24-FEB-1997; 97US-0038253P.  
XX PA (THER-) THERION BIOLOGICS CORP.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA (DAND ) DANA FARBER CANCER INST INC.  
XX PI Schlom J, Kantor J, Kufe D, Panicali D, Gritz L;  
XX WPI; 1998-467492/40.  
XX DR New recombinant pox virus for tumour therapy - comprises DNA encoding an  
PT immunogenic mini-MUC1 fragment comprising 5-25 MUC1 tandem repeat units.  
XX PS Disclosure; Page 11; 42pp; English.  
XX CC The MUC1 tandem repeat units AAV48317-V48325 were used to create an  
CC immunogenic mini-MUC1 fragment for inclusion in a recombinant pox virus  
CC (RPV). The RPV was used in a pharmaceutical composition also containing  
CC an immunomodulator to generate MUC1 specific cytotoxic T-lymphocytes. The  
CC recombinant pox virus therefore encodes an immunogenic MUC1 fragment that  
CC does not undergo significant genetic deletion, thereby providing an  
CC unexpectedly stable and immunogenic pox virus. They can be used to  
CC prevent or treat tumours expressing MUC1 tumour-associated antigens  
XX  
SQ Sequence 60 BP; 7 A; 29 C; 19 G; 5 T; 0 U; 0 Other;  
XX  
Alignment Scores:  
Pred. No.: 6.26e-06 Length: 60  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0  
US-10-057-136-1 (1-20) x AAV48318 (1-60)  
QY 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
Db 1 GGATCCACCGCGCGCGCTCGGCACGGAGTGACGTGGGCGCCGACACGCGCCGCTCCC 60  
RESULT 7  
AAV48323  
ID AAV48323 standard; DNA; 60 BP.  
XX  
AC AAV48323;  
XX  
DT 20-NOV-1998 (first entry)  
XX  
DE Nucleotide sequence encoding MUC1 tandem repeat unit R8.  
XX  
KW ss; MUC1; recombinant pox virus; cytotoxic T-lymphocyte; immunogen;  
KW tumour; tumour-associated antigen.  
XX  
OS Homo sapiens.  
XX  
PN WO9837095-A2.  
XX  
PD 27-AUG-1998.  
XX  
PF 24-FEB-1998; 98WO-US003693.  
XX  
PR 24-FEB-1997; 97US-0038253P.  
XX  
PA (THER-) THERION BIOLOGICS CORP.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA (DAND ) DANA FARBER CANCER INST INC.  
XX  
PI Schlom J, Kantor J, Kufe D, Panicali D, Gritz L;

XX WPI; 1998-467492/40.  
XX New recombinant pox virus for tumour therapy - comprises DNA encoding an  
PT immunogenic mini-MUC1 fragment comprising 5-25 MUC1 tandem repeat units.  
XX PS Disclosure; Page 11; 42pp; English.  
XX CC The MUC1 tandem repeat units AAV48317-V48325 were used to create an  
CC immunogenic mini-MUC1 fragment for inclusion in a recombinant pox virus  
CC (RPV). The RPV was used in a pharmaceutical composition also containing  
CC an immunomodulator to generate MUC1 specific cytotoxic T-lymphocytes. The  
CC recombinant pox virus therefore encodes an immunogenic MUC1 fragment that  
CC does not undergo significant genetic deletion, thereby providing an  
CC unexpectedly stable and immunogenic pox virus. They can be used to  
CC prevent or treat tumours expressing MUC1 tumour-associated antigens  
XX  
SQ Sequence 60 BP; 10 A; 24 C; 17 G; 9 T; 0 U; 0 Other;  
XX  
Alignment Scores:  
Pred. No.: 6.26e-06 Length: 60  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0  
US-10-057-136-1 (1-20) x AAV48323 (1-60)  
QY 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
Db 1 GGGTCGACTGCCCTCCGGCGCATGGTGTGACCTCAGTCTCTGACACACAGGCCAGCCCCA 60  
RESULT 8  
AAV48316  
ID AAV48316 standard; cDNA; 60 BP.  
XX  
AC AAV48316;  
XX  
DT 20-NOV-1998 (first entry)  
XX  
DE Nucleotide sequence encoding MUC1 tandem repeat unit.  
XX  
KW ss; MUC1; recombinant pox virus; cytotoxic T-lymphocyte; immunogen;  
KW tumour; tumour-associated antigen.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..60  
FT /\*tag= 'a  
FT /product= "MUC1 tandem repeat unit"  
XX  
PN WO9837095-A2.  
XX  
PD 27-AUG-1998.  
XX  
PF 24-FEB-1998; 98WO-US003693.  
XX  
PR 24-FEB-1997; 97US-0038253P.  
XX  
PA (THER-) THERION BIOLOGICS CORP.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PA (DAND ) DANA FARBER CANCER INST INC.  
XX  
PI Schlom J, Kantor J, Kufe D, Panicali D, Gritz L;  
XX WPI; 1998-467492/40.  
XX P-PSDB; AAW77229.  
XX  
PT New recombinant pox virus for tumour therapy - comprises DNA encoding an  
PT immunogenic mini-MUC1 fragment comprising 5-25 MUC1 tandem repeat units.  
XX

Example 1; Page 20; 42pp; English.

The MUC1 tandem repeat unit was used to create an immunogenic mini-MUC1 fragment for inclusion in a recombinant pox virus (RPV). The RPV was used in a pharmaceutical composition also containing an immunomodulator to generate MUC1 specific cytotoxic T-lymphocytes. The recombinant pox virus therefore encodes an immunogenic MUC1 fragment that does not undergo significant genetic deletion, thereby providing an unexpectedly stable and immunogenic pox virus. They can be used to prevent or treat tumours expressing MUC1 tumour-associated antigens

Sequence 60 BP; 7 A; 33 C; 16 G; 4 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 6.26e-06 Length: 60  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-057-136-1 (1-20) x AAV48316 (1-60)

1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
|||||  
1 GGCTCCACCGCCCCCCCCAGCCAGGTGTACCTGGCCCCCGACACACCGGCCCG 60

RESULT 9

AAV48319  
ID AAV48319 standard; DNA; 60 BP.

AAV48319;

20-NOV-1998 (first entry)

Nucleotide sequence encoding MUC1 tandem repeat unit R4.

ss; MUC1; recombinant pox virus; cytotoxic T-lymphocyte; immunogen; tumour; tumour-associated antigen.

Homo sapiens.

WO9837095-A2.

27-AUG-1998.

24-FEB-1998; 98WO-US003693.

24-FEB-1997; 97US-0038253P.

(THER-) THERION BIOLOGICS CORP.  
(USSH ) US DEPT HEALTH & HUMAN SERVICES.  
(DAND ) DANA FARBER CANCER INST INC.

Schlom J, Kantor J, Kufe D, Panicali D, Gritz L;

WPI; 1998-467492/40.

New recombinant pox virus for tumour therapy - comprises DNA encoding an immunogenic mini-MUC1 fragment comprising 5-25 MUC1 tandem repeat units.

Disclosure; Page 11; 42pp; English.

The MUC1 tandem repeat units AAV48317-V48325 were used to create an immunogenic mini-MUC1 fragment for inclusion in a recombinant pox virus (RPV). The RPV was used in a pharmaceutical composition also containing an immunomodulator to generate MUC1 specific cytotoxic T-lymphocytes. The recombinant pox virus therefore encodes an immunogenic MUC1 fragment that does not undergo significant genetic deletion, thereby providing an unexpectedly stable and immunogenic pox virus. They can be used to prevent or treat tumours expressing MUC1 tumour-associated antigens

Sequence 60 BP; 10 A; 23 C; 13 G; 14 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 6.26e-06 Length: 60  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-057-136-1 (1-20) x AAV48319 (1-60)

1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
|||||  
1 GGGTCAACAGCTCCTCCCGCTCATGGGGTTACTTCTGCTCCAGATACTCGCCAGCTCCA 60

RESULT 10

AAV48317

ID AAV48317 standard; DNA; 60 BP.

AAV48317;

20-NOV-1998 (first entry)

Nucleotide sequence encoding MUC1 tandem repeat unit R2.

ss; MUC1; recombinant pox virus; cytotoxic T-lymphocyte; immunogen; tumour; tumour-associated antigen.

Homo sapiens.

WO9837095-A2.

27-AUG-1998.

24-FEB-1998; 98WO-US003693.

24-FEB-1997; 97US-0038253P.

(THER-) THERION BIOLOGICS CORP.  
(USSH ) US DEPT HEALTH & HUMAN SERVICES.  
(DAND ) DANA FARBER CANCER INST INC.

Schlom J, Kantor J, Kufe D, Panicali D, Gritz L;

WPI; 1998-467492/40.

New recombinant pox virus for tumour therapy - comprises DNA encoding an immunogenic mini-MUC1 fragment comprising 5-25 MUC1 tandem repeat units.

Disclosure; Page 11; 42pp; English.

The MUC1 tandem repeat units AAV48317-V48325 were used to create an immunogenic mini-MUC1 fragment for inclusion in a recombinant pox virus (RPV). The RPV was used in a pharmaceutical composition also containing an immunomodulator to generate MUC1 specific cytotoxic T-lymphocytes. The recombinant pox virus therefore encodes an immunogenic MUC1 fragment that does not undergo significant genetic deletion, thereby providing an unexpectedly stable and immunogenic pox virus. They can be used to prevent or treat tumours expressing MUC1 tumour-associated antigens

Sequence 60 BP; 17 A; 21 C; 13 G; 9 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 6.26e-06 Length: 60  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 2 Gaps: 0

US-10-057-136-1 (1-20) x AAV48317 (1-60)

1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20

```
Db      |||||||
1 GGCAGTACTGCACCAACCGGCATGGCGTAAACATCAGCACCTGATACAGACCTGCACCT 60

RESULT 11
ADK68635/c
ID      ADK68635 standard; cDNA; 156 BP.
XX
AC      ADK68635;
XX
DT      06-MAY-2004 (first entry)
XX
DE      HSP65-MUC1 antigen CTL epitope related cDNA #3.
XX
KW      Human breast cancer; Mycobacterium bovis; heat shock protein 65; BCG;
KW      HSP65; cytotoxic T lymphocyte; CTL; MUC1; HSP65-MUC1 antigen CTL epitope;
KW      ss.
XX
OS      Unidentified.
XX
PN      CN1368384-A.
XX
PD      11-SEP-2002.
XX
PF      08-FEB-2001; 2001CN-00102614.
XX
PR      08-FEB-2001; 2001CN-00102614.
XX
PA      (DIWE-) DIWEIHUAYU BIO TECHNOLOGY CO LTD BEIJING.
XX
PI      Yu Y, Li H;
XX
WPI; 2003-854662/80.
XX
SQ      Genetically engineered vaccine of MUC-1 antigen for human breast cancer.
XX
PS      Example 2; Page 4 (Disclosure); 14pp; Chinese.
XX
CC      The invention relates to a method of preparation of a genetically
CC      engineered vaccine for preventing and treating human breast cancer. The
CC      method comprises fusing the coding gene of the Mycobacterium bovis heat
CC      shock protein 65 (BCG HSP65) with the cytotoxic T lymphocyte (CTL)
CC      epitope gene of MUC1 (antigen cell expressed by human breast cancer
CC      cells) and the HSP65-MUC1 antigen CTL epitope is expressed in Escherichia
CC      coli cells. This sequence represents DNA used in the method of the
CC      invention.
XX
SQ      Sequence 156 BP; 37 A; 42 C; 58 G; 19 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      1.72e-05      Length:      156
Score:          109.00      Matches:      20
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:     100.00%      Indels:      0
DB:            10      Gaps:        0

US-10-057-136-1 (1-20) x ADK68635 (1-156)

Qy      1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db      132 GGTTCACCGCTCCGCGGCTCAGGTGTACTCTGCTCCGGACACCCGTCGGGCTCCG 73

RESULT 12
AAN90579/c
ID      AAN90579 standard; cDNA; 309 BP.
XX
AC      AAN90579;
XX
DT      27-AUG-2003 (revised)
DT      25-MAR-2003 (revised)
DT      04-DEC-1989 (first entry)
XX
DE      pdf9.3 cDNA insert.
```

```
XX      pdf9.3; human DF3 breast carcinoma-associated antigen epitope.
KW      Human MCF-7 breast carcinoma cells; 'ATCC HTB22'.
XX      WO8907107-A.
XX      10-AUG-1989.
XX      29-JAN-1988; 88US-00149831.
XX      29-JAN-1988; 88US-00149831.
PR      (DANA-) DANA-FARBER CANCER.
XX      Kufe DW;
XX      WPI; 1989-248989/34.
DR      P-PSDB; AAP91045, AAP91053, AAP91054, AAP90146.
XX      Recombinant polypeptide(s) - contains DF 3 breast carcinoma antigen
PT      epitope and useful as assay reagents, and encoding DNA sequences.
XX      Claim 1; Fig 4; 31pp; English.
XX      The sequence encodes a carbohydrate-free polypeptide contg. DF3 breast
CC      carcinoma antigen epitope. Useful as a competitive binding assay reagent
CC      and improves diagnosis. The cDNA consists of nearly identical 60 BP
CC      tandem repeats which are 85% GC-rich. See also AAP91045, AAP91046,
CC      AAP91053, AAP91054. (Updated on 25-MAR-2003 to correct PA field.)
CC      (Updated on 27-AUG-2003 to correct OS field.)
XX      SQ      Sequence 309 BP; 21 A; 92 C; 160 G; 36 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      3.54e-05      Length:      309
Score:          109.00      Matches:      20
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:     100.00%      Indels:      0
DB:            1      Gaps:        0

US-10-057-136-1 (1-20) x AAN90579 (1-309)

Qy      1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20
Db      266 GGCTCCACCGCCCCCCAGCCACGGGTGCACCTCGGCCCGGACACCCAGCGCCCCCG 207

RESULT 13
AAD00385
ID      AAD00385 standard; DNA; 525 BP.
XX
AC      AAD00385;
XX      29-AUG-2000 (first entry)
DT
XX      Human Mucin 1 (MUC-1) protein fragment encoding DNA #2.
DE
XX      Human; Mucin 1; MUC-1; tumour; pMRS30 expression vector; anti-tumour;
KW      therapy; immune response; cytostatic; vaccine; ds.
XX      Homo sapiens.
OS
XX      Key      Location/Qualifiers
FT      CDS      1..525
FT      /*tag= a
FT      /product= "MUC-1 protein fragment"
XX
PN      WO200025827-A2.
XX      11-MAY-2000.
XX      18-OCT-1999; 99WO-EP007874.
PF
```



XX 30-OCT-1998; 98IT-MI002330.  
XX (MENA ) MENARINI RICERCHE SPA.  
XX PI Parente D, Di Massimo AM, De Santis R;  
XX WPI; 2000-365410/31.  
DR P-PSDB; AAY71021.  
XX Composition containing one or more DNA molecules encoding fragments of a  
PT Mucin 1 (MUC-1) protein overexpressed in tumor cells, useful in anti-  
PT tumor therapy.  
XX Claim 16; Fig 2; 56pp; English.  
XX The present sequence is a DNA encoding a fragment of human Mucin 1 (MUC-  
CC 1) antigenic protein which is overexpressed in tumour cells. The sequence  
CC was obtained from BR20 tumour cells by reverse transcriptase- PCR and  
CC corresponds to nucleotides 205-720 of the EMBL sequence J05581 with a  
CC start codon and two stop codons. The present sequence is cloned into a  
CC pMRS30 expression vector and used in pharmaceutical composition e.g.  
CC vaccine for inducing an antigen-specific anti-tumour immune response.  
CC Composition containing this DNA molecule is useful in anti-tumour therapy  
CC of patients affected with tumours characterised by high MUC-1 expression  
XX SQ Sequence 525 BP; 111 A; 199 C; 128 G; 87 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 6.2e-05 Length: 525  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0  
  
US-10-057-136-1 (1-20) x AAD00385 (1-525)  
  
QY 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
Db 256 GGAAGTACTGCTCCACCAGCACACGGTGTACTCTCGGCTCCGGATACCAGGCGGCCCA 315  
  
RESULT 14  
AAD00391  
ID AAD00391 standard; DNA; 891 BP.  
XX  
AC AAD00391;  
XX  
DT 15-SEP-2003 (revised)  
DT 29-AUG-2000 (first entry)  
XX  
DE Ubiquitin-E. coli LacI-human Mucin 1 fusion protein encoding DNA #2.  
XX  
KW Ubiquitin; LacI; beta-galactosidase; fusion protein; human; Mucin 1;  
KW MUC-1; tumour; pMRS30 expression vector; anti-tumour; therapy;  
KW immune response; cytostatic; vaccine; ds.  
XX  
OS Homo sapiens.  
OS Escherichia coli.  
OS Chimeric.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..891  
FT /\*tag= a  
FT /product= "Ubiquitin-LacI-MUC-1 fusion protein"  
FT misc\_feature 1..369  
FT /\*tag= b  
FT /label= UBILacI\_DNA  
FT /note= "Includes ubiquitin-E. coli LacI fusion DNA"  
FT misc\_feature 370..891  
FT /\*tag= c  
FT /note= "Human MUC-1 partial DNA that corresponds to  
FT nucleotides 205-720 of the EMBL sequence J05581 with two

FT stop codons"  
XX  
PN WO200025827-A2.  
XX  
PD 11-MAY-2000.  
XX  
PF 18-OCT-1999; 99WO-EP007874.  
XX  
PR 30-OCT-1998; 98IT-MI002330.  
XX  
PA (MENA ) MENARINI RICERCHE SPA.  
XX  
PI Parente D, Di Massimo AM, De Santis R;  
XX  
DR WPI; 2000-365410/31.  
DR P-PSDB; AAY71027.  
XX  
XX Composition containing one or more DNA molecules encoding fragments of a  
PT Mucin 1 (MUC-1) protein overexpressed in tumor cells, useful in anti-  
PT tumor therapy.  
XX Claim 18; Fig 8; 56pp; English.  
XX The present sequence is a DNA encoding a fusion protein consisting of  
CC human Mucin 1 (MUC-1) fragment fused to UBILacI sequence at the N-  
CC terminus. The UBILacI sequence consists of ubiquitin from MCF7 cell line  
CC and a portion of E. coli beta-galactosidase (LacI). MUC-1 is an antigenic  
CC protein overexpressed in tumor cells. The present sequence is cloned  
CC into a pMRS30 expression vector and used in pharmaceutical composition  
CC e.g. vaccine for inducing an antigen-specific anti-tumour immune  
CC response. Composition containing this DNA molecule is useful in anti-  
CC tumour therapy of patients affected with tumours characterised by high  
CC MUC-1 expression. (Updated on 15-SEP-2003 to standardise OS field)  
XX SQ Sequence 891 BP; 203 A; 307 C; 225 G; 156 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 0.000109 Length: 891  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0  
  
US-10-057-136-1 (1-20) x AAD00391 (1-891)  
  
QY 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
Db 622 GGAAGTACTGCTCCACCAGCACACGGTGTACTCTCGGCTCCGGATACCAGGCGGCCCA 681  
  
RESULT 15  
ADI57712  
ID ADI57712 standard; cDNA; 1194 BP.  
XX  
AC ADI57712;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE Human breast specific nucleic acid (BSNA) #83.  
XX  
KW Human; breast specific nucleic acid; BSNA; gene; ss; metastasis;  
KW breast cancer; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN WO2003106648-A2.  
XX  
PD 24-DEC-2003.  
XX  
PF 16-JUN-2003; 2003WO-US018934.  
XX  
PR 14-JUN-2002; 2002US-0389327P.  
XX

PA (DIAD-) DIADEXUS INC.  
XX  
PI Salceda S, Macina RA, Turner LR, Sun Y, Liu C;  
XX  
DR WPI; 2004-082185/08.  
DR P-PSDB; ADI57782.  
XX  
PT Novel isolated polypeptide comprising breast specific protein sequences,  
PT useful for diagnosing or monitoring presence and metastases of breast  
PT cancer in patient.  
XX  
PS Claim 1; SEQ ID NO 83; 370pp; English.  
XX  
CC The invention relates to human breast specific nucleic acids (BSNA) and  
CC the breast specific proteins (BSP) they encode. The nucleic acids are  
CC useful for determining the presence of a BSNA in a sample which involves  
CC contacting the sample with a BSNA under conditions in which the BSNA will  
CC selectively hybridise to a BSNA in the sample, and detecting the  
CC hybridisation. The nucleic acids are useful for determining the presence  
CC of a BSP in a sample which involves contacting the sample with suitable  
CC reagent under conditions in which the reagent will selectively interact  
CC with the BSP, and detecting the interaction of the reagent with a BSP in  
CC the sample. The nucleic acids and proteins are useful for diagnosing or  
CC monitoring the presence and metastases of breast cancer in a patient,  
CC which involves determining an amount of nucleic acid or protein and  
CC comparing the determined amount of nucleic acid or protein in the sample  
CC of the patient to the amount of a breast specific marker in a normal  
CC control, where a difference in the determined amount in the sample  
CC compared to the amount in the control is associated with the presence of  
CC breast cancer. The sequences are useful for treating a patient with  
CC breast cancer, involving administering a composition consisting of a BSNA  
CC or a BSP to a patient, where the administration induces an immune  
CC response against the breast cancer cell expressing the BSNA or BSP. This  
CC sequence represents a human BSNA of the invention.  
XX  
SQ Sequence 1194 BP; 243 A; 438 C; 275 G; 238 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 0.000148 Length: 1194  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 12 Gaps: 0

US-10-057-136-1 (1-20) x ADI57712 (1-1194)

QY 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
Db 596 GGCTCCACCGCCCCCCCCAGCCACGGTGTACCTCGGCCCGGACACACGCGGCCCG 655

Search completed: June 30, 2005, 08:07:38  
Job time : 363 secs



GenCore version 5.1.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 30, 2005, 06:42:59 ; Search time 2603 Seconds  
(without alignments)  
372.303 Million cell updates/sec

Title: US-10-057-136-1

Perfect score: 109

Sequence: 1 GSTAPPAGHGVTSAPDTRPAP 20

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/cgn2 1/USPTO spool/US10057136/runat 29062005 162122 11390/app query.fasta\_1.199  
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10057136@cgn 1 1 3731@runat 29062005 162122 11390 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:\*

1: gb\_ba:\*  
2: gb\_hgt:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	109	100.0	120	6 AX192396	AX192396 Sequence
C 2	109	100.0	120	6 BD000571	BD000571 Human pol
C 3	109	100.0	525	6 BD225141	BD225141 Medicinal
C 4	109	100.0	891	6 BD225147	BD225147 Medicinal

5	109	100.0	1371	6	BD225144	BD225144 Medicinal
6	109	100.0	1414	12	AF423031	AF423031 Synthetic
7	109	100.0	1455	6	CQ715242	CQ715242 Sequence
8	109	100.0	1457	6	AX959914	AX959914 Sequence
9	109	100.0	1737	6	BD225150	BD225150 Medicinal
10	109	100.0	1774	6	AX959684	AX959684 Sequence
11	109	100.0	1774	6	AX959912	AX959912 Sequence
12	109	100.0	1800	6	CQ875507	CQ875507 Sequence
13	109	100.0	1804	6	AR492318	AR492318 Sequence
14	109	100.0	1804	6	AX335367	AX335367 Sequence
15	109	100.0	1804	9	HUMMUCAB	J05581 Human polym
16	109	100.0	1818	6	CQ875500	CQ875500 Sequence
17	109	100.0	1818	6	CQ875505	CQ875505 Sequence
18	109	100.0	1834	12	AF423030	AF423030 Synthetic
19	109	100.0	1835	6	AX959918	AX959918 Sequence
20	109	100.0	2135	6	AX959916	AX959916 Sequence
21	109	100.0	2297	6	BD272907	BD272907 A recombi
22	109	100.0	4139	6	CQ834017	CQ834017 Sequence
23	109	100.0	4139	6	AX334899	AX334899 Sequence
24	109	100.0	4139	6	AX335372	AX335372 Sequence
25	109	100.0	4139	6	AX336712	AX336712 Sequence
26	109	100.0	4139	6	AX409474	AX409474 Sequence
27	109	100.0	4139	6	AX440481	AX440481 Sequence
28	109	100.0	4139	9	HUMPANMU	J05582 Human pancr
29	109	100.0	7188	9	AY463543	AY463543 Homo sapi
30	109	100.0	8181	6	AX406624	AX406624 Sequence
31	109	100.0	8181	9	HUMPEM	M61170 Human polym
32	109	100.0	8186	6	AR492320	AR492320 Sequence
33	109	100.0	133525	9	AL711399	AL711399 Human DNA
34	104	95.4	1572	6	AX093798	AX093798 Sequence
35	104	95.4	1721	6	CQ771290	CQ771290 Sequence
36	104	95.4	1721	6	AR492306	AR492306 Sequence
37	104	95.4	1721	6	AX335860	AX335860 Sequence
38	104	95.4	1721	6	AX440427	AX440427 Sequence
39	104	95.4	1721	6	AX587588	AX587588 Sequence
40	104	95.4	1721	9	HSTEYMA	X52229 Human mRNA
41	104	95.4	1971	6	AX963157	AX963157 Sequence
42	104	95.4	2037	6	AX963159	AX963159 Sequence
43	104	95.4	2238	9	HSSETA	X52228 Human mRNA
44	102	93.6	491	9	HUMEPISIBI	M32739 Human episi
45	102	93.6	518	6	AR492402	AR492402 Sequence

ALIGNMENTS

RESULT 1	AX192396/c	AX192396	120 bp	DNA	linear	PAT 15-AUG-2001
LOCUS	Sequence 2 from Patent EP1103623.					
DEFINITION	AX192396					
ACCESSION	AX192396.1	GI:15210363				
VERSION						
KEYWORDS						
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1					
AUTHORS	Taylor-Papadimitriou, J., Burchell, J. and Gendler, S.					
TITLE	Human mucin core protein: nucleic acid probes, peptide fragments and antibodies thereto, and uses thereof in diagnostic and therapeutic methods					
JOURNAL	Patent: EP 1103623-A 2 30-MAY-2001;					
	IMPERIAL CANCER RESEARCH TECHNOLOGY LIMITED (GB)					
FEATURES	Location/Qualifiers					
source	1..120					
	/organism="Homo sapiens"					
	/mol_type="unassigned DNA"					
	/db_xref="taxon:9606"					

ORIGIN

Alignment Scores: 0.000133 Length: 120  
Pred. No.: 109.00 Matches: 20  
Score:

Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-057-136-1 (1-20) x AX192396 (1-120)

Qy 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
|||||  
Db 87 GGCTCCACCGCCCCCAGCCACGGTGTCACTCGGCCCGGACACCAGCGGCCCG 28

RESULT 2  
BD000571/c 120 bp DNA linear PAT 31-JAN-2002  
LOCUS Human polymorphic epithelial mucin core protein and nucleic acid  
DEFINITION encoding the protein.  
ACCESSION BD000571  
VERSION BD000571.1 GI:18623684  
KEYWORDS JP 2000333675-A/2.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 120)  
AUTHORS Papadimitrov,J.T., Jendora,S. and Bachieru,J.  
TITLE Human polymorphic epithelial mucin core protein and nucleic acid  
encoding the protein  
JOURNAL Patent: JP 2000333675-A 2 05-DEC-2000;  
IMPERIAL CANCER RESEARCH TECHNOLOGY LTD  
COMMENT OS Homo sapiens (human)  
PN JP 2000333675-A/2  
PD 05-DEC-2000  
PF 26-APR-2000 JP 2000125724  
PR 07-JAN-1987 GB 8700269,07-JAN-1987 GB 8700279 PR  
22-APR-1987 US 041306,09-NOV-1987 GB 8726172 PI JOYCE  
TAYLOR PAPADIMITROV,SANDRA JENDORA,JOY BACHIERU PC  
C12N15/02,A61K38/00,A61K39/395,A61K49/00,A61P35/00, PC  
C07K14/47,  
PC C07K16/44,C12N5/10,C12P21/08/(C12N15/02,C12R1:91),(C12N5/10,  
PC C12R1:91),  
PC C12N15/00,A61K37/02,C12N5/00,(C12N15/00,C12R1:91),(C12N5/00,  
PC C12R1:91)  
CC  
FH Key Location/Qualifiers  
FT source 1..120  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

FEATURES  
source Location/Qualifiers  
1..120  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Alignment Scores: 0.000133 Length: 120  
Pred. No.: 109.00 Matches: 20  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 100.00% Gaps: 0  
DB: 6

US-10-057-136-1 (1-20) x BD000571 (1-120)

Qy 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
|||||  
Db 87 GGCTCCACCGCCCCCAGCCACGGTGTCACTCGGCCCGGACACCAGCGGCCCG 28

RESULT 3  
BD225141 525 bp DNA linear PAT 17-JUL-2003  
LOCUS Medicinal composition having antitumor effect and containing DNA  
DEFINITION encoding antigenic protein.  
ACCESSION BD225141

VERSION BD225141.1 GI:33034911  
KEYWORDS JP 2002528519-A/2.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 525)  
AUTHORS Pallente,D., Massimo,A.M.D. and Desantis,R.  
TITLE Medicinal composition having antitumor effect and containing DNA  
encoding antigenic protein  
JOURNAL Patent: JP 2002528519-A 2 03-SEP-2002;  
MENARINI RICERCHE SPA  
COMMENT OS Homo sapiens (human)  
PN JP 2002528519-A/2  
PD 03-SEP-2002  
PF 18-OCT-1999 JP 2000579265  
PR 30-OCT-1998 IT MI98A002330  
PI DINO PALLENTE,ANNA MARIA D MASSIMO,RITA DESANTIS PC  
A61K38/00,A61K35/76,A61K39/00,A61K48/00,A61P35/00,C12N15/09, PC  
A61K37/02,  
PC C12N15/00  
CC Medicinal composition having antitumor effect and containing  
DNA encoding  
CC antigenic protein  
FH Key Location/Qualifiers  
FT source 1..525  
/organism="Homo sapiens (human)"

FEATURES  
source Location/Qualifiers  
1..525  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Alignment Scores: 0.000486 Length: 525  
Pred. No.: 109.00 Matches: 20  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 100.00% Gaps: 0  
DB: 6

US-10-057-136-1 (1-20) x BD225141 (1-525)

Qy 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
|||||  
Db 256 GGAAGTACTGCTCCACCAGCACACGGTGTACCTCGGCTCCGATACCGCGGCCCA 315

RESULT 4  
BD225147 891 bp DNA linear PAT 17-JUL-2003  
LOCUS Medicinal composition having antitumor effect and containing DNA  
DEFINITION encoding antigenic protein.  
ACCESSION BD225147  
VERSION BD225147.1 GI:33034917  
KEYWORDS JP 2002528519-A/8.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 891)  
AUTHORS Pallente,D., Massimo,A.M.D. and Desantis,R.  
TITLE Medicinal composition having antitumor effect and containing DNA  
encoding antigenic protein  
JOURNAL Patent: JP 2002528519-A 8 03-SEP-2002;  
MENARINI RICERCHE SPA  
COMMENT OS Homo sapiens (human)  
PN JP 2002528519-A/8  
PD 03-SEP-2002  
PF 18-OCT-1999 JP 2000579265  
PR 30-OCT-1998 IT MI98A002330  
PI DINO PALLENTE,ANNA MARIA D MASSIMO,RITA DESANTIS PC  
A61K38/00,A61K35/76,A61K39/00,A61K48/00,A61P35/00,C12N15/09, PC

A61K37/02,  
PC C12N15/00  
CC Medicinal composition having antitumor effect and containing  
CC DNA encoding  
CC antigenic protein  
FH Key Location/Qualifiers  
FT source 1. .891  
FT /organism='Homo sapiens (human)'.  
FT Location/Qualifiers  
1. .891  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

FEATURES  
source

ORIGIN

Alignment Scores:  
Pred. No.: 0.000774 Length: 891  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-057-136-1 (1-20) x BD225147 (1-891)

QY 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
|||||  
DB 622 GGAAGTACTGCTCCACCAGCACACGGTGTACCTCGGCTCCGGATACCAGGCGGCCCA 681

RESULT 5

BD225144

LOCUS

DEFINITION BD225144 1371 bp DNA linear PAT 17-JUL-2003  
Medicinal composition having antitumor effect and containing DNA  
encoding antigenic protein.

ACCESSION BD225144

VERSION BD225144.1 GI:33034914

KEYWORDS JP 2002528519-A/5.

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS Pallente,D., Massimo,A.M.D. and Desantis,R.  
TITLE Medicinal composition having antitumor effect and containing DNA  
encoding antigenic protein

JOURNAL

COMMENT Patent: JP 2002528519-A 5 03-SEP-2002;

MENARINI RICERCH SPA

OS Homo sapiens (human)

PN JP 2002528519-A/5

PD 03-SEP-2002

PF 18-OCT-1999 JP 2000579265

PR 30-OCT-1998 IT MI98A002330

PI DINO PALLENTE,ANNA MARIA D MASSIMO,RITA DESANTIS PC

A61K38/00,A61K35/76,A61K39/00,A61K48/00,A61P35/00,C12N15/09, PC

A61K37/02,

PC C12N15/00

CC Medicinal composition having antitumor effect and containing  
CC DNA encoding

CC antigenic protein

FH Key Location/Qualifiers

FT source 1. .1371  
FT /organism='Homo sapiens (human)'.  
FT Location/Qualifiers

1. .1371

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

FEATURES

source

ORIGIN

Alignment Scores:  
pred. No.: 0.00113 Length: 1371  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-057-136-1 (1-20) x BD225144 (1-1371)

QY 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
|||||  
DB 325 GGAAGTACCCTCCACCAGCACACGGTGTACCTCGGCTCCGGATACCAGGCGGCCCA 384

RESULT 6

AF423031

LOCUS

DEFINITION AF423031 1414 bp mRNA linear SYN 10-JUL-2003  
Synthetic construct Homo sapiens mucin variant MUC1-CT58 (MUC1)  
mRNA, complete cds; alternatively spliced.

ACCESSION AF423031

VERSION AF423031.1 GI:19338621

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1 other sequences; artificial sequences.

AUTHORS Hinojosa-Kurtzberg,A.M., Johansson,M.E., Madsen,C.S., Hansson,G.C.  
and Gendler,S.J.

TITLE Novel MUC1 splice variants contribute to mucin overexpression in  
CFTR-deficient mice

JOURNAL Am. J. Physiol. Gastrointest. Liver Physiol. 284 (5), G853-G862  
(2003)

MEDLINE 22570517

PUBMED 12529261

REFERENCE 2 (bases 1 to 1414)

AUTHORS Hinojosa-Kurtzberg,A.M. and Gendler,S.J.

TITLE Direct Submission

JOURNAL Submitted (21-SEP-2001) Biochemistry, Mayo Clinic, 13400 E. Shea  
Boulevard, Scottsdale, AZ 85259, USA

FEATURES Location/Qualifiers

1. .1414

/organism="synthetic construct"

/mol\_type="mRNA"

/db\_xref="taxon:32630"

/note="Homo sapiens gene in transgenic Mus musculus  
C57BL/6; isolated from intestinal mucosa"

1. .1414

/gene="MUC1"

1. .1386

/gene="MUC1"

/note="alternatively spliced; contains exon 6b resulting  
in variant carboxy-terminal domain; lacks sites for  
beta-catenin and Grb2 interactions; derived from Homo  
sapiens"

/codon\_start=1

/transl\_table=11

/product="mucin variant MUC1-CT58"

/protein\_id="AAL86735.1"

/db\_xref="GI:19338622"

/translation="MTPTQTSPFFLLLLTLVTVTSGHASSTPGGEKETSATQRSS  
VPSSTEKNVAMTSSVLSHSPGSGSSTTQGDVTLAPATEPASGSAATWQDVTSVP  
VTRPALGSTTPPAHDVTSAPDNKPAGSTAPPAHGVTSAPDTRPAPGSTAPPAHGVTS  
APDNRPALGSTAPPVHNVTASGASGASASTLVHNGTSARATTTTTPASKSTPFSIPSHH  
SDPTTTLASHSTKTDASTHSTVPLTSSNHSSTPQLSTGVFFLSFHISNLQFNS  
SLEDPTDYYQELQDISFMFLQIYKGGFLGSLNIFKRPGSVVVQLTLAFREGTINV  
HDVETQFNQYKTEAASRYNLTISDVSDVDFPFPSAQSGAGVPGWGIALLVLVCVLVA  
LAIVYLIALAVCCQCRKNYQLDIFPARDTYHPMSEYPTYHTHGRVVPSPSTDSPYE  
KEWRVDRERLA"

ORIGIN

Alignment Scores:

Pred. No.: 0.00116 Length: 1414

Score: 109.00 Matches: 20

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 12 Gaps: 0

US-10-057-136-1 (1-20) x AF423031 (1-1414)

Qy 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
Db 385 GGCTCCACCGCCCCCAGCCACGGTGTACCTCGGCCCGGACACCGCGGCCCG 444

RESULT 7  
CQ715242  
LOCUS CQ715242 1455 bp DNA linear PAT 03-FEB-2004  
DEFINITION Sequence 1176 from Patent WO02068579.  
ACCESSION CQ715242  
VERSION CQ715242.1 GI:42276099  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE  
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.  
TITLE Kits, such as nucleic acid arrays, comprising a majority of  
humanexons or transcripts, for detecting expression and other uses  
thereof  
JOURNAL Patent: WO 02068579-A 1176 06-SEP-2002;  
PE Corporation (NY) (US)  
FEATURES  
source Location/Qualifiers  
1. .1455  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Alignment Scores:  
Pred. No.: 0.00119 Length: 1455  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-057-136-1 (1-20) x CQ715242 (1-1455)

Qy 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
Db 412 GGCTCCACCGCCCCCAGCCACGGTGTACCTCGGCCCGGACACCGCGGCCCG 471

RESULT 8  
AX959914  
LOCUS AX959914 1457 bp DNA linear PAT 14-JAN-2004  
DEFINITION Sequence 19 from Patent WO03100060.  
ACCESSION AX959914  
VERSION AX959914.1 GI:40880143  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE  
AUTHORS Burden, N.G., Ellis, J.H. and Hamblin, P.A.  
TITLE Muc-1 antigen with reduced number of vnter repeat units  
JOURNAL Patent: WO 03100060-A 19 04-DEC-2003;  
GLAXO GROUP LIMITED (GB)  
FEATURES  
source Location/Qualifiers  
1. .1457  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Alignment Scores:  
Pred. No.: 0.00119 Length: 1457  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-057-136-1 (1-20) x AX959914 (1-1457)

Qy 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
Db 403 GGCTCCACCGCCCCCAGCCACGGTGTACCTCGGCCCGGACACCGCGGCCCG 462

RESULT 9  
BD225150  
LOCUS BD225150 1737 bp DNA linear PAT 17-JUL-2003  
DEFINITION Medicinal composition having antitumor effect and containing DNA  
encoding antigenic protein.  
ACCESSION BD225150  
VERSION BD225150.1 GI:33034920  
KEYWORDS JP 2002528519-A/11.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1737)  
REFERENCE  
AUTHORS Pallente, D., Massimo, A.M.D. and Desantis, R.  
TITLE Medicinal composition having antitumor effect and containing DNA  
encoding antigenic protein  
JOURNAL Patent: JP 2002528519-A 11 03-SEP-2002;  
MENARINI RICERCHE SPA  
COMMENT OS Homo sapiens (human)  
PN JP 2002528519-A/11  
PD 03-SEP-2002  
PF 18-OCT-1999 JP 2000579265  
PR 30-OCT-1998 IT MI98A002330  
PI DINO PALLEENTE, ANNA MARIA D MASSIMO, RITA DESANTIS PC  
A61K38/00, A61K35/76, A61K39/00, A61K48/00, A61P35/00, C12N15/09, PC  
A61K37/02,  
PC C12N15/00  
CC Medicinal composition having antitumor effect and containing  
CC DNA encoding  
CC antigenic protein  
FH Key Location/Qualifiers  
FT source 1. .1737  
/organism="Homo sapiens (human)"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Alignment Scores:  
Pred. No.: 0.00139 Length: 1737  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-057-136-1 (1-20) x BD225150 (1-1737)

Qy 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
Db 691 GGAAGTACCGCTCCACCAGCACACGGTGTACCTCGGTCGGATACCAGCGGCCCGCA 750

RESULT 10  
AX959684  
LOCUS AX959684 1774 bp DNA linear PAT 14-JAN-2004  
DEFINITION Sequence 10 from Patent WO03099193.  
ACCESSION AX959684  
VERSION AX959684.1 GI:40880030  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1  
AUTHORS Burden,N. and Hamblin,P.  
TITLE Vaccines  
JOURNAL Patent: WO 0309193-A 10 04-DEC-2003;  
GLAXO GROUP LIMITED (GB)

## FEATURES

source  
1. .1774  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Alignment Scores:  
Pred. No.: 0.00142 Length: 1774  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-057-136-1 (1-20) x AX959684 (1-1774)

QY 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
|||||  
Db 462 GGCTCCACCGCCCCCGCCAGCCACGGTGTACCTCGGCCCGGACACCGCGGCCCG 521

## RESULT 11

AX959912  
LOCUS AX959912 1774 bp DNA linear PAT 14-JAN-2004  
DEFINITION Sequence 17 from Patent WO03100060.  
ACCESSION AX959912  
VERSION AX959912.1 GI:40880142

## KEYWORDS

Source Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1  
AUTHORS Burden,N.G., Ellis,J.H. and Hamblin,P.A.  
TITLE Muc-1 antigen with reduced number of vnt repeat units  
JOURNAL Patent: WO 03100060-A 17 04-DEC-2003;  
GLAXO GROUP LIMITED (GB)

## FEATURES

source  
1. .1774  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Alignment Scores:  
Pred. No.: 0.00142 Length: 1774  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-057-136-1 (1-20) x AX959912 (1-1774)

QY 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
|||||  
Db 462 GGCTCCACCGCCCCCGCCAGCCACGGTGTACCTCGGCCCGGACACCGCGGCCCG 521

## RESULT 12

CQ875507  
LOCUS CQ875507 1800 bp DNA linear PAT 27-SEP-2004  
DEFINITION Sequence 16 from Patent WO2004076665.  
ACCESSION CQ875507  
VERSION CQ875507.1 GI:52748471

## KEYWORDS

Source synthetic construct

ORGANISM synthetic construct  
other sequences; artificial sequences.

## REFERENCE

1  
AUTHORS Hamblin,P.A. and Rocha Del Cura,M.D.  
TITLE Vaccines derived from epithelial cell mucin muc-1  
JOURNAL Patent: WO 2004076665-A 16 10-SEP-2004;  
GLAXO GROUP LIMITED (GB)

## FEATURES

Location/Qualifiers  
1. .1800  
/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="codon modified DNA"

## ORIGIN

Alignment Scores:  
Pred. No.: 0.00144 Length: 1800  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-057-136-1 (1-20) x CQ875507 (1-1800)

QY 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
|||||  
Db 391 GGCTCCACCGCCCCCGCCAGCCACGGTGTACCTCGGCCCGGACACCGCGGCCCG 450

## RESULT 13

AR492318  
LOCUS AR492318 1804 bp DNA linear PAT 15-MAY-2004  
DEFINITION Sequence 17 from patent US 6716627.  
ACCESSION AR492318  
VERSION AR492318.1 GI:47260892

## KEYWORDS

Source Unknown.

## ORGANISM

Unclassified.

REFERENCE 1 (bases 1 to 1804)

AUTHORS Dobie,K.W.

TITLE Antisense modulation of mucin 1, transmembrane expression

JOURNAL Patent: US 6716627-A 17 06-APR-2004;

## FEATURES

Location/Qualifiers  
1. .1804  
/organism="unknown"  
/mol\_type="genomic DNA"

## ORIGIN

Alignment Scores:  
Pred. No.: 0.00144 Length: 1804  
Score: 109.00 Matches: 20  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-057-136-1 (1-20) x AR492318 (1-1804)

QY 1 GlySerThrAlaProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
|||||  
Db 457 GGCTCCACCGCCCCCGCCAGCCACGGTGTACCTCGGCCCGGACACCGCGGCCCG 516

## RESULT 14

AX335367  
LOCUS AX335367 1804 bp DNA linear PAT 09-JAN-2002  
DEFINITION Sequence 5876 from Patent WO0194629.  
ACCESSION AX335367  
VERSION AX335367.1 GI:18126086

## KEYWORDS

Source Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,  
Horrigan,S., Soppet,D.R. and Weaver,Z.  
TITLE Cancer gene determination and therapeutic screening using signature  
gene sets  
JOURNAL Patent: WO 0194629-A 5876 13-DEC-2001;  
Avalon Pharmaceuticals (US)  
FEATURES Location/Qualifiers  
source 1..1804  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
  
ORIGIN  
Alignment Scores: 0.00144 Length: 1804  
Pred. No.: 109.00 Matches: 20  
Score: 109.00  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
  
US-10-057-136-1 (1-20) x AX335367 (1-1804)  
  
Qy 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
|||||  
Db 457 GGCTCCACCGCCCCCCCCAGCCACGGGTGTACCTCGGCCCGGACACACCGCGGCCCG 516  
  
RESULT 15  
HUMMUCAB 1804 bp mRNA linear PRI 07-JAN-1995  
LOCUS Human polymorphic epithelial mucin (PEM) mRNA, complete cds.  
DEFINITION J05581  
ACCESSION J05581  
VERSION J05581.1 GI:188869  
KEYWORDS polymorphic epithelial mucin.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1804)  
AUTHORS Gendler,S.J., Lancaster,C.A., Taylor-Papadimitriou,J., Duhig,T.,  
Peat,N., Burchell,J., Pemberton,L., Ialoni,E.N. and Wilson,D.  
TITLE Molecular cloning and expression of human tumor-associated  
polymorphic epithelial mucin  
JOURNAL J. Biol. Chem. 265 (25), 15286-15293 (1990)  
MEDLINE 90368715  
PUBMED 1697589  
COMMENT Original source text: Homo sapiens adult adenocarcinoma cDNA to  
mRNA.  
Draft entry and computer-readable sequence for [J. Biol. Chem.  
(1990) In press] kindly submitted  
by S.J.Gendler, 26-JUN-1990.  
FEATURES Location/Qualifiers  
source 1..1804  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/map="Xq26.3-q27.1"  
/cell\_line="BT20"  
/tissue\_type="adenocarcinoma"  
/dev\_stage="adult"  
1..1804  
/gene="MCNAA"  
<1..1804  
/gene="MCNAA"  
/product="PEM mRNA"  
73..1500  
/gene="MCNAA"  
/codon\_start=1  
/product="polymorphic epithelial mucin"  
/protein\_id="AA59876.1"  
/db\_xref="GI:188870"

/translation="MTPGTQSPFFLLLLLTVLTVVTGSGHASSTPGGEKETSATQRSS  
VPSSTEKNAVSMTSSVLSSHSPGSGSTTQGDVTLAPATEPASGSAATWGQDVTSPV  
VTRPALGSTTTPAHADVTAPDNKPAPGSTAPPAHGVTSAPDTRPAPGSTAPPAGHVTIS  
APDNRPALGSTAPPVHNVTASGSASASTLVHNGTSARATTPASKSTPFSIPSHH  
SDTPTTLASHSTKTDASSTHSTVPPLTSSNHSTSPQLSTGVSTFFFLSFHISNLQFNS  
SLEDPSDYVQELQRDISEMFLQIYKQGGFLGSLNFKRPGSVVQVLTTLAFREGTINV  
HDVETQFNQYKTEAASRYNLTISDVSVSDVPPFSAQSAGVPCWGIALLLVLCVLVA  
LAIVYLIALAVCQCRKNYGOLDIFPARDTYHPMSEYPTYHTHGRYVPPSPSTDSPYE  
KVSAGNGGSSLSYTNPAVAATSANL"  
73..135  
/gene="MCNAA"  
136..1497  
/gene="MCNAA"  
/product="polymorphic epithelial mucin"  
1783..1788  
/gene="MCNAA"  
  
sig\_peptide  
mat\_peptide  
polyA\_signal  
  
ORIGIN  
Alignment Scores: 0.00144 Length: 1804  
Pred. No.: 109.00 Matches: 20  
Score: 109.00  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0  
  
US-10-057-136-1 (1-20) x HUMMUCAB (1-1804)  
  
Qy 1 GlySerThrAlaProProAlaHisGlyValThrSerAlaProAspThrArgProAlaPro 20  
|||||  
Db 457 GGCTCCACCGCCCCCCCCAGCCACGGGTGTACCTCGGCCCGGACACACCGCGGCCCG 516  
  
Search completed: June 30, 2005, 08:01:32  
Job time : 2608 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 30, 2005, 05:41:13 ; Search time 345 Seconds  
(without alignments)  
29.686 Million cell updates/sec

Title: US-10-057-136-1

Perfect score: 109

Sequence: 1 GSTAPPAHGVTSPADTRPAP 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	109	100.0	1255	1	MUC1_HUMAN	P15941 h mucin 1 p
2	94	86.2	475	1	MUC1_HYLLA	Q29435 hylobates 1
3	93	85.3	256	2	Q7M4M7	Q7m4m7 homo sapien
4	74	67.9	553	2	Q9MZL1	Q9mzl1 macaca mula
5	68	62.4	20	2	Q9UM18	Q9umi8 homo sapien
6	59	54.1	745	2	Q89X06	Q89x06 bradyrhizob
7	58.5	53.7	1334	2	Q9RKR9	Q9rkr9 streptomyce
8	56	51.4	654	2	Q8X1F0	Q8x1f0 cryptococcu
9	56	51.4	779	2	Q6FTP1	Q6ftp1 candida gla
10	55	50.5	933	2	Q6M2Z6	Q6mzz6 homo sapien
11	55	50.5	1339	2	Q9ULK3	Q9ulk3 homo sapien
12	54	49.5	276	2	Q6UX35	Q6ux35 homo sapien
13	54	49.5	282	2	Q81YJ0	Q8iyj0 homo sapien
14	54	49.5	282	2	Q95K74	Q95k74 macaca fasc
15	54	49.5	282	2	Q9N088	Q9n088 macaca fasc
16	54	49.5	290	2	Q6ESR4	Q6esr4 oryza sativ
17	54	49.5	403	2	Q42417	Q42417 gallus gall
18	54	49.5	558	2	Q82IR8	Q82ir8 streptomyce
19	54	49.5	628	1	ASH2_HUMAN	Q9ub13 homo sapien
20	54	49.5	705	2	Q7SEF5	Q7sfns neurospora
21	53	48.6	355	2	Q73ZH6	Q73zh6 mycobacteri
22	53	48.6	584	2	Q8XC6	Q8xc6 ralstonia s
23	53	48.6	673	2	Q8V725	Q8v725 cercopithec
24	53	48.6	673	2	Q7T5C3	Q7t5c3 cercopithec
25	53	48.6	823	2	Q6DKA9	Q6dka9 xenopus lae
26	52	47.7	157	2	Q82E38	Q82e38 streptomyce
27	52	47.7	188	2	Q7W0D8	Q7w0d8 bordetella
28	52	47.7	244	2	Q8Z690	Q8z690 salmonella
29	52	47.7	244	2	Q8ZP19	Q8zpl9 salmonella
30	52	47.7	360	2	Q7QJ16	Q7qj16 anopheles g
31	52	47.7	406	2	Q8VPM8	Q8vpm8 micrococcus

RESULT 1									
MUC1_HUMAN									
ID	MUC1_HUMAN	STANDARD;	PRT;	1255	AA.				
AC	P15941; P13931; P15942; P17626; Q14128; Q14876; Q16437; Q16442;								Q6pk46 homo sapien
AC	Q16615; Q9BXA4; Q9UE75; Q9UE76; Q9UQL1; Q9Y4J2;								Q7tsc9 mus musculu
DT	01-JAN-1990 (Rel. 13, Created)								P31503 rattus norv
DT	01-APR-1990 (Rel. 14, Last sequence update)								Q7tsd0 mus musculu
DT	25-OCT-2004 (Rel. 45, Last annotation update)								P15143 gallus gall
DE	Mucin 1 precursor (MUC-1) (Polymorphic epithelial mucin) (PEM) (PEMT) (Episialin) (Tumor-associated mucin) (Carcinoma-associated mucin)								P14859 homo sapien
DE	(Tumor-associated epithelial membrane antigen) (EMA) (H23AG) (Peanut-reactive urinary mucin) (PUM) (Breast carcinoma-associated antigen								Q29076 sus scrofa
DE	DF3) (CD227 antigen).								P25425 mus musculu
GN	Name=MUC1;								Q8bt04 mus musculu
OS	Homo sapiens (Human).								Q7sd01 neurospora
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								Q92xj0 bacterioph
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								Q8yqj7 anabaena sp
OX	NCBI_TaxID=9606;								Q8y3a4 ralstonia s
RN	[1]								Q924x8 streptomyce
RP	SEQUENCE FROM N.A. (ISOFORM 1).								
RC	TISSUE=Pancreas;								
RX	MEDLINE=90368716; PubMed=2394722;								
RA	Lan M.S., Batra S.K., Qi W.-N., Metzgar R.S., Hollingsworth M.A.;								
RL	"Cloning and sequencing of a human pancreatic tumor mucin cDNA.";								
RN	J. Biol. Chem. 265:15294-15299(1990).								
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).								
RX	MEDLINE=90202794; PubMed=2318825;								
RA	Ligtenberg M.J.L., Vos H.L., Gennissen A.M.C., Hilkens J.;								
RT	"Episialin, a carcinoma-associated mucin, is generated by a								
RT	polymorphic gene encoding splice variants with alternative amino								
RT	termini.";								
RL	J. Biol. Chem. 265:5573-5578(1990).								
RN	[3]								
RP	SEQUENCE FROM N.A. (ISOFORM 1).								
RC	TISSUE=Breast carcinoma;								
RX	MEDLINE=90368715; PubMed=1697589;								
RA	Gendler S.J., Lancaster C.A., Taylor-Papadimitriou J., Duhig T.,								
RA	Peat N., Burchell J., Pemberton L., Lalani E.-N., Wilson D.;								
RT	"Molecular cloning and expression of human tumor-associated								
RT	polymorphic epithelial mucin.";								
RL	J. Biol. Chem. 265:15286-15293(1990).								
RN	[4]								
RP	SEQUENCE FROM N.A. (ISOFORM 1).								
RX	MEDLINE=91097524; PubMed=2268309;								
RA	Lancaster C.A., Peat N., Duhig T., Wilson D., Taylor-Papadimitriou J.,								
RA	Gendler S.J.;								
RT	"Structure and expression of the human polymorphic epithelial mucin								
RT	gene: an expressed VNTR unit.";								
RL	Biochem. Biophys. Res. Commun. 173:1019-1029(1990).								
RN	[5]								
RP	SEQUENCE FROM N.A. (ISOFORM 5).								
RC	TISSUE=Breast carcinoma;								
RX	MEDLINE=90276413; PubMed=2351132;								

ALIGNMENTS

RA Wreschner D.H., Hareuveni M., Tsarfaty I., Smorodinsky N., Horev J.,  
RA Zaretsky J., Kotkes P., Weiss M., Lathe R., Dion A., Keydar I.,  
RT "Human epithelial tumor antigen CDNA sequences. Differential splicing  
RL may generate multiple protein forms.";  
RL Eur. J. Biochem. 189:463-473(1990).  
RN [6]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Breast carcinoma;  
RX MEDLINE=90276414; PubMed=2112460;  
RA Hareuveni M., Tsarfaty I., Zaretsky J., Kotkes P., Horev J.,  
RA Zrihan S., Weiss M., Green S., Lathe R., Keydar I., Wreschner D.H.;  
RT "A transcribed gene, containing a variable number of tandem repeats,  
RT codes for a human epithelial tumor antigen. cDNA cloning, expression  
RT of the transfected gene and over-expression in breast cancer tissue.";  
RL Eur. J. Biochem. 189:475-486(1990).  
RN [7]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX MEDLINE=91033045; PubMed=1688329; DOI=10.1016/0378-1119(90)90242-J;  
RA Tsarfaty I., Hareuveni M., Horev J., Zaretsky J., Weiss M.,  
RA Jeltsch J.M., Garnier J.M., Lathe R., Keydar I., Wreschner D.H.;  
RT "Isolation and characterization of an expressed hypervariable gene  
RT coding for a breast-cancer-associated antigen.";  
RL Gene 93:313-318(1990).  
RN [8]  
RP SEQUENCE FROM N.A. (ISOFORM 7).  
RX MEDLINE=95010060; PubMed=7925397;  
RA Zrihan-Licht S., Vos H.L., Baruch A., Elroy-Stein O., Sagiv D.,  
RA Keydar I., Hilkens J., Wreschner D.H.;  
RT "Characterization and molecular cloning of a novel MUC1 protein,  
RT devoid of tandem repeats, expressed in human breast cancer tissue.";  
RL Eur. J. Biochem. 224:787-795(1994).  
RN [9]  
RP SEQUENCE FROM N.A. (ISOFORMS 6; 7 AND 8).  
RX MEDLINE=97355747; PubMed=9212228;  
RA Oosterkamp H.M., Scheiner L., Stefanova M.C., Lloyd K.O.,  
RA Finstad C.L.;  
RT "Comparison of MUC-1 mucin expression in epithelial and non-epithelial  
RT cancer cell lines and demonstration of a new short variant form (MUC-  
RT 1/Z)." ;  
RL Int. J. Cancer 72:87-94(1997).  
RN [10]  
RP SEQUENCE FROM N.A. (ISOFORM 7), AND VARIANT MET-1117.  
RA Zhang L.X., Li C.H.;  
RT "Molecular cloning of an isoform of MUC1, MUC1/Y." ;  
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
RN [11]  
RP SEQUENCE FROM N.A. (ISOFORM 9).  
RC TISSUE=Epithelial cancer;  
RA Zhang L.X., Li C.H., Sun L.Y., Yue W.;  
RT "Cloning of a new potential secreted short variant form of MUC1 mucin  
RT in epithelial cancer cell line." ;  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
RN [12]  
RP SEQUENCE FROM N.A. (ISOFORM 8), AND VARIANTS MET-1117 AND ASN-1142.  
RA Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.,  
RA Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S.,  
RA Sherwood J.K., Leithauser B.J., Nickerson D.A.;  
RT "NIEHS-SNPs, environmental genome project, NIEHS ES15478, Department  
RT of Genome Sciences, Seattle, WA (URL: <http://egp.gs.washington.edu>).";  
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
RN [13]  
RP PARTIAL SEQUENCE FROM N.A.  
RX MEDLINE=88330762; PubMed=3417635;  
RA Gendler S.J., Taylor-Papadimitriou J., Duhig T., Rothbard J.,  
RA Burchell J.;  
RT "A highly immunogenic region of a human polymorphic epithelial mucin  
RT expressed by carcinomas is made up of tandem repeats." ;  
RL J. Biol. Chem. 263:12820-12823(1988).  
RN [14]  
RP SEQUENCE OF 1-160 FROM N.A. (ISOFORM 2).  
RX MEDLINE=9008473; PubMed=2597151;  
RA Abe M., Siddiqui J., Kufe D.;  
RT "Sequence analysis of the 5' region of the human DF3 breast carcinoma-

RT associated antigen gene." ;  
RL Biochem. Biophys. Res. Commun. 165:644-649(1989).  
RN [15]  
RP SEQUENCE OF 1-109 FROM N.A. (ISOFORM 2).  
RC TISSUE=Thyroid;  
RX MEDLINE=96183746; PubMed=8608966;  
RA Weiss M., Baruch A., Keydar I., Wreschner D.H.;  
RT "Preoperative diagnosis of thyroid papillary carcinoma by reverse  
RT transcriptase polymerase chain reaction of the MUC1 gene." ;  
RL Int. J. Cancer 66:55-59(1996).  
RN [16]  
RP SEQUENCE OF 1-89 FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=96181716; PubMed=8604237;  
RA Yu C.J., Yang P.C., Shew J.Y., Hong T.M., Yang S.C., Lee Y.C.,  
RA Lee L.N., Luh K.T., Wu C.W.;  
RT "Mucin mRNA expression in lung adenocarcinoma cell lines and  
RT tissues." ;  
RL Oncology 53:118-126(1996).  
RN [17]  
RP SEQUENCE OF 1-46 FROM N.A. (ISOFORMS 3 AND 4).  
RC TISSUE=Breast carcinoma;  
RA Buluwela L., Liu Q., Lugmani Y.A., Gomm J.J., Coombes R.C.;  
RL Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.  
RN [18]  
RP CARBOHYDRATE-LINKAGE SITES WITHIN THE REPEAT.  
RX MEDLINE=97460054; PubMed=9312074; DOI=10.1074/jbc.272.40.24780;  
RA Mueller S., Goletz S., Packer N., Gooley A.A., Lawson A.M.,  
RA Hanisch F.-G.;  
RT "Localization of O-glycosylation sites on glycopeptide fragments from  
RT lactation-associated MUC1. All putative sites within the tandem repeat  
RT are glycosylation targets in vivo." ;  
RL J. Biol. Chem. 272:24780-24793(1997).  
RN [19]  
RP CARBOHYDRATE-LINKAGE SITES WITHIN THE REPEAT.  
RX MEDLINE=99303572; PubMed=10373415; DOI=10.1074/jbc.274.26.18165;  
RA Mueller S., Alving K., Peter-Katalinic J., Zachara N., Gooley A.A.,  
RA Hanisch F.-G.;  
RT "High density O-glycosylation on tandem repeat peptide from secretory  
RT MUC1 of T47D breast cancer cells." ;  
RL J. Biol. Chem. 274:18165-18172(1999).  
RN [20]  
RP POLYMORPHISM WITHIN THE REPEAT.  
RX MEDLINE=21359366; PubMed=11350974; DOI=10.1074/jbc.M103187200;  
RA Engelmann K., Baldus S.E., Hanisch F.-G.;  
RT "Identification and topology of variant sequences within individual  
RT repeat domains of the human epithelial tumor mucin MUC1." ;  
RL J. Biol. Chem. 276:27764-27769(2001).  
RN [21]  
RP CHARACTERIZATION OF ISOFORM Y, AND MUTAGENESIS OF ASP-1116.  
RX MEDLINE=99211485; PubMed=10197628;  
RA Baruch A., Hartmann M.-L., Yoeli M., Adereth Y., Greenstein S.,  
RA Stadler Y., Skornik Y., Zaretsky J., Smorodinsky N.I., Keydar I.,  
RA Wreschner D.H.;  
RT "The breast cancer-associated MUC1 gene generates both a receptor and  
RT its cognate binding protein." ;  
RL Cancer Res. 59:1552-1561(1999).  
RN [22]  
RP PARTIAL SEQUENCE, AND CHARACTERIZATION OF CLEAVAGE SITE.  
RX MEDLINE=21240104; PubMed=11341784; DOI=10.1006/bbrc.2001.4775;  
RA Parry S., Silverman H.S., McDermott K., Willis A., Hollingsworth M.A.,  
RA Harris A.;  
RT "Identification of MUC1 proteolytic cleavage sites in vivo." ;  
RL Biochem. Biophys. Res. Commun. 283:715-720(2001).  
RN [23]  
RP CHARACTERIZATION.  
RX MEDLINE=21836452; PubMed=11847293; DOI=10.1110/ps.16502;  
RA Wreschner D.H., McGuckin M.A., Williams S.J., Baruch A., Yoeli M.,  
RA Ziv R., Okun L., Zaretsky J., Smorodinsky N., Keydar I., Neophytou P.,  
RA Stacey M., Lin H.-H., Gordon S.;  
RT "Generation of ligand-receptor alliances by 'SEA' module-mediated  
RT cleavage of membrane-associated mucin proteins." ;  
RL Protein Sci. 11:698-706(2002).



```
RN [24]
RP PHOSPHORYLATION.

Query Match      100.0%; Score 109; DB 1; Length 1255;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSTAPPAHGVTSAPDTRPAP 20
DB 129 GSTAPPAHGVTSAPDTRPAP 148

RESULT 2
MUC1_HYLLA
ID MUC1_HYLLA STANDARD; PRT; 475 AA.
AC Q29435;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Mucin 1 precursor (MUC-1).
GN Name=MUC1;
OS Hylobates lar (Common gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hylobatidae; Hylobates.
OC NCBI_TaxID=9580;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96351712; PubMed=8747930;
RA Spicer A.P., Duhig T., Chilton B.S., Gendler S.J.;
RT "Analysis of mammalian MUC1 genes reveals potential functionally
important domains."
RL Mamm. Genome 6:885-888(1995).
CC -!- FUNCTION: Direct or indirect interaction with actin cytoskeleton
CC -!- (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- PTM: Highly O-glycosylated and probably also N-glycosylated.
CC -!- SIMILARITY: Contains 1 SEA domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L41589; AAA69965.1; --
CC EMBL; L41625; AAA69918.1; --
CC EMBL; L41624; AAA69918.1; JOINED.
CC InterPro; IPR000082; SEA.
CC Pfam; PF01390; SEA; 1.
CC SMART; SM00200; SEA; 1.
CC PROSITE; PS50024; SEA; 1.
KW Actin-binding; Cytoskeleton; Glycoprotein; Repeat; Signal;
KW Transmembrane.
FT SIGNAL 1 23 Potential.
FT CHAIN 24 475 Mucin 1.
FT DOMAIN 24 380 Extracellular (Potential).
FT TRANSMEM 381 401 Potential.
FT DOMAIN 402 475 Cytoplasmic (Potential).
FT REPEAT 102 121 1.
FT REPEAT 122 141 2.
FT REPEAT 142 161 3.
FT REPEAT 162 181 4.
FT DOMAIN 254 371 SEA.
SQ SEQUENCE 475 AA; 49371 MW; D7A699D6D68C6622 CRC64;

Query Match      86.2%; Score 94; DB 1; Length 475;
Best Local Similarity 94.4%; Pred. No. 0.00037;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSTAPPAHGVTSAPDTRP 18
||||| |||||||
```

```
DB 129 GSTAPPAHGVTSAPDTRP 146

RESULT 3
Q7M4M7
ID Q7M4M7 PRELIMINARY; PRT; 256 AA.
AC Q7M4M7;
DT 01-MAR-2004 (TrEMBLrel.. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tumor-associated antigen DF3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90058554; PubMed=2582438;
RA Merlo G.R., Siddiqui J., Cropp C.S., Liscia D.S., Lidereau R.,
RA Callahan R., Kufe D.W.;
RT "Frequent alteration of the DF3 tumor-associated antigen gene in
primary human breast carcinomas.";
RL Cancer Res. 49:6966-6971(1989).
DR PIR; A60533; A60533.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR GO; GO:0019068; P:Viral assembly; IEA.
DR InterPro; IPR000982; Matrix.
DR ProDom; PD000741; Matrix; 2.
DR SEQUENCE 256 AA; 25766 MW; E0430F0BA7F30B04 CRC64;

Query Match      85.3%; Score 93; DB 2; Length 256;
Best Local Similarity 85.0%; Pred. No. 0.00027;
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GSTAPPAHGVTSAPDTRPAP 20
DB 12 GSTAPPAHRTSAPESRPAP 31
||||| ||||||| |||||:|||||

RESULT 4
Q9MZL1
ID Q9MZL1 PRELIMINARY; PRT; 553 AA.
AC Q9MZL1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mucin 1 (Fragment).
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OC NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20330533; PubMed=10869775; DOI=10.1016/S0264-410X(00)00143-2;
RA Vaughan H.A., Ho D.W.M., Karanikas V., Sandrin M.S., McKenzie I.F.C.,
RA Pietersz G.A.;
RT "The immune response of mice and cynomolgus monkeys to macaque mucin
1-mannan.";
RL Vaccine 18:3297-3309(2000).
DR EMBL; AF176947; AAF82403.1; --
DR InterPro; IPR000082; SEA.
DR Pfam; PF01390; SEA; 1.
DR SMART; SM00200; SEA; 1.
DR PROSITE; PS50024; SEA; 1.
FT NON_TER 1 553
FT NON_TER 553
SQ SEQUENCE 553 AA; 55778 MW; 6D7E6DD2EE929318 CRC64;

Query Match      67.9%; Score 74; DB 2; Length 553;
Best Local Similarity 75.0%; Pred. No. 0.18;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

QY 1 GSTAPPAHGVTSAPDTRPAP 20  
107 GSTGPPARVVTSAPDTSAP 126

Db

RESULT 5  
Q9UMI8  
ID Q9UMI8 PRELIMINARY; PRT; 20 AA.  
AC Q9UMI8;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Mucin (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89235154; PubMed=2715633;  
RA Xing P.X., Tjandra J.J., Reynolds K., McLaughlin P.J., Purcell D.F.J.,  
RA McKenzie I.F.C.;  
RT "Reactivity of anti-human milk fat globule antibodies with synthetic  
peptides";  
RL J. Immunol. 142:3503-3509(1989).  
DR EMBL; M26316; AAA36336.1; -.  
DR PIR; S10571; S10571.  
FT NON\_TER 1  
FT NON\_TER 20  
SQ SEQUENCE 20 AA; 1887 MW; 5B3473EAEBAFAD87 CRC64;

Query Match 62.4%; Score 68; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 0.037;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSTAPPAHGVTS 13  
8 GSTAPPAHGVTS 20

Db

RESULT 6  
Q89X06  
ID Q89X06 PRELIMINARY; PRT; 745 AA.  
AC Q89X06;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Blr0521 protein.  
GN OrderedLocusNames=blr0521;  
OS Bradyrhizobium japonicum.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Bradyrhizobiaceae; Bradyrhizobium.  
OX NCBI\_TaxID=375;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=USDA110;  
MEDLINE=22484998; PubMed=12597275;  
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,  
RA Sasamoto S., Watanabe A., Idesawa K., Iiguchi M., Kawashima K.,  
RA Kohara M., Matsumoto M., Shimpō S., Tsuruoka H., Wada T., Yamada M.,  
RA Tabata S.;  
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium  
Bradyrhizobium japonicum USDA110.";  
RL DNA Res. 9:189-197(2002).  
DR EMBL; AP005936; BAC45786.1; -.  
DR HSSP; P07176; 1OAP.  
DR GO:00092279; C:outer membrane (sensu Gram-negative Bacteria); IEA.  
DR GO:00051199; F:structural constituent of cell wall; IEA.  
DR InterPro; IPR006665; OmpA/MotB.  
DR InterPro; IPR003882; Pistil\_extensin.  
DR Pfam; PF00691; OmpA; 1.  
DR PRINTS; PR01218; PSTIEXTENSIN.  
DR ProDom; PD000930; OmpA/MotB; 1.

KW Complete proteome.  
SQ SEQUENCE 745 AA; 74544 MW; 155EDFCC74DBC6D CRC64;

Query Match 54.1%; Score 59; DB 2; Length 745;  
Best Local Similarity 64.7%; Pred. No. 22;  
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 APPAHGVTSAPDTRPAP 20  
269 SPPAPGATPAPTTPAP 285

Db

RESULT 7  
Q9RKR9  
ID Q9RKR9 PRELIMINARY; PRT; 1334 AA.  
AC Q9RKR9;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Putative multi-domain regulatory protein.  
GN ORFNames=SCC75A.05c;  
OS Streptomyces coelicolor.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1902;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=A3(2) / M145;  
MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;  
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,  
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,  
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S.,  
RA Rabinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,  
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,  
RA Hopwood D.A.;  
RT "Complete genome sequence of the model actinomycete Streptomyces  
coelicolor A3(2).";  
RL Nature 417:141-147(2002).  
DR EMBL; AL939112; CAB61705.1; -.  
DR PIR; T50568; T50568.  
DR GO:0003677; F:DNA binding; IEA.  
DR GO:0000156; F:two-component response regulator activity; IEA.  
DR GO:0042829; P:defense response to pathogen; IEA.  
DR GO:0000160; P:two-component signal transduction system (p. . .; IEA.  
DR InterPro; IPR009059; bi\_resp\_regltr\_C.  
DR InterPro; IPR005158; BTAD.  
DR InterPro; IPR00767; Disease\_resist.  
DR InterPro; IPR008941; TPR-like.  
DR InterPro; IPR01867; Trans\_reg\_C.  
DR Pfam; PF03704; BTAD; 1.  
DR Pfam; PF00486; Trans\_reg\_C; 1.  
DR PRINTS; PR00364; DISEASERSIST.  
DR ProDom; PD000329; Trans\_reg\_C; 1.  
KW Complete proteome.  
SQ SEQUENCE 1334 AA; 138786 MW; 78DC746883E8778C CRC64;

Query Match 53.7%; Score 58.5; DB 2; Length 1334;  
Best Local Similarity 68.4%; Pred. No. 45;  
Matches 13; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 2 STAPPAHGVTSAPDTRPAP 20  
328 STAPP-HDTASAADTAPAP 345

Db

RESULT 8  
Q8X1F0  
ID Q8X1F0 PRELIMINARY; PRT; 654 AA.  
AC Q8X1F0;  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE PAK1 kinase.  
OS Cryptococcus neoformans var. neoformans.  
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;  
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.  
OX NCBI\_TaxID=40410;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22343357; PubMed=12455960; DOI=10.1128/EC.1.2.257-272.2002;  
RA Wang P., Nichols C.B., Lengeler K.B., Cardenas M.E., Cox G.M.,  
RA Perfect J.R., Heitman J.;  
RT "Mating-type-specific and nonspecific PAK kinases play shared and  
divergent roles in Cryptococcus neoformans.";  
RL Eukaryotic Cell 1:257-272(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Breeding C.S., Lengeler K.B., Wang P., Heitman J.;  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
DR EMBL: AF391151; AAL58842.1; -.  
DR HSSP: Q13153; 1F3M.  
DR GO: GO:0005524; F:ATP binding; IEA.  
DR GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO: GO:0016740; F:transferase activity; IEA.  
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR Pfam: PF00786; PBD; 1.  
DR Pfam: PF00069; Pkinase; 1.  
DR ProDom: PD000001; Prot\_kinase; 1.  
DR SMART: SM00285; PBD; 1.  
DR SMART: SM00220; S\_TK; 1.  
DR PROSITE: PS50108; CRIB; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; UNKNOWN\_1.  
DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 654 AA; 71267 MW; DCEFA16AB4PB9215 CRC64;  
  
Query Match 51.4%; Score 56; DB 2; Length 654;  
Best Local Similarity 62.5%; Pred. No. 47;  
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
  
QY 5 PPAHGVTSAAPDTRPAP 20  
Db 251 PPPHTSSAPPTAPAP 266  
  
RESULT 9  
Q6FTP1 ID Q6FTP1 PRELIMINARY; PRT; 779 AA.  
AC Q6FTP1;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Similar to sp|P37370 Saccharomyces cerevisiae YLR337c VRP1.  
GN ORFNames=CAGL0G00968g;  
OS Candida glabrata CBS138.  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.  
OX NCBI\_TaxID=284593;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CBS138;  
RG Genolevures;  
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,  
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talia E.,  
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,  
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,  
RA Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,  
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,  
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,  
RA Nicaud J.M., Nikolski M., Oztas S., Ozler-Kalogeropoulos O.,

RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,  
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,  
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,  
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,  
RA Wincker P., Souciet J.L.;  
RT "Genome evolution in yeasts.";  
RL Nature 430:35-44(2004).  
DR EMBL: CR380953; CAG59330.1; -.  
DR InterPro: IPR003124; WH2.  
DR Pfam: PF02205; WH2; 2.  
DR SMART: SM00246; WH2; 2.  
SQ SEQUENCE 779 AA; 75743 MW; C850564PBF43156E CRC64;  
  
Query Match 51.4%; Score 56; DB 2; Length 779;  
Best Local Similarity 64.7%; Pred. No. 56;  
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
  
QY 4 APPAHGVTSAAPDTRPAP 20  
Db 419 APPAPSMTSAPPAPAP 435  
  
RESULT 10  
Q6MZZ6 ID Q6MZZ6 PRELIMINARY; PRT; 933 AA.  
AC Q6MZZ6;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein DKFZp686E0469.  
GN Name=DKFZp686E0469;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human endometrium carcinoma cell line;  
RG The German Human cDNA Consortium;  
RA Ansoerge W., Krieger S., Regiert T., Rittmueller C., Schwager B.,  
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BX640796; CAE45879.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 933 AA; 102860 MW; 188A7B37EC84669B CRC64;  
  
Query Match 50.5%; Score 55; DB 2; Length 933;  
Best Local Similarity 45.0%; Pred. No. 90;  
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;  
  
QY 1 GSTAPPAHGVTSAAPDTRPAP 20  
Db 19 GSTAHPHPAIPNSPPSTPVP 38  
  
RESULT 11  
Q9ULK3 ID Q9ULK3 PRELIMINARY; PRT; 1339 AA.  
AC Q9ULK3;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE KIAA1217 protein (Fragment).  
GN Name=KIAA1217;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=20039619; PubMed=10574462;  
RA Nagase T., Ishikawa K., Kikuno R., Hirose M., Nomura N., Ohara O.;

RT "Prediction of the coding sequences of unidentified human genes. XV.  
RT The complete sequences of 100 new cDNA clones from brain which code  
RT for large proteins in vitro."  
RL DNA Res. 6:337-345(1999).  
DR EMBL; AB033043; BAA86531.2; -.  
FT NON TER 1  
SQ SEQUENCE 1339 AA; 146176 MW; 47448505314E8A56 CRC64;  
  
Query Match 50.5%; Score 55; DB 2; Length 1339;  
Best Local Similarity 45.0%; Pred. No. 1.3e+02;  
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;  
  
QY 1 GSTAPPAHGVTSAPDTRPAP 20  
Db ||||| : : : : :  
296 GSTAHPHPAIPNSPPSTPVP 315  
  
RESULT 12  
Q6UX35 PRELIMINARY; PRT; 276 AA.  
ID Q6UX35;  
AC Q6UX35;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE ESRM828.  
GN ORFNames=UNQ828;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;  
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,  
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,  
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,  
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,  
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
RA Godowski P.;  
RT "The secreted protein discovery initiative (SPDI), a large-scale  
RT effort to identify novel human secreted and transmembrane proteins: a  
RT bioinformatics assessment."  
RL Genome Res. 13:2265-2270(2003).  
DR EMBL; AV358534; AAQ8898.1; -.  
SQ SEQUENCE 276 AA; 29426 MW; 72C81C7DF9B7CB89 CRC64;  
  
Query Match 49.5%; Score 54; DB 2; Length 276;  
Best Local Similarity 62.5%; Pred. No. 36;  
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
  
QY 5 PPAHGVTSAPDTRPAP 20  
Db ||||| : : : : :  
27 PPAQGSSSSPRTPPAP 42  
  
RESULT 13  
Q8IYJ0 PRELIMINARY; PRT; 282 AA.  
ID Q8IYJ0;  
AC Q8IYJ0;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Hypothetical protein DKFZp547D2210.  
GN Name=DKFZp547D2210;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.

RC TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Strausberg R.;  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBSJ databases.  
DR EMBL; BC035736; AAH35736.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 282 AA; 30076 MW; 772F37069CE472C8 CRC64;  
  
Query Match 49.5%; Score 54; DB 2; Length 282;  
Best Local Similarity 62.5%; Pred. No. 36;  
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
  
Qy 5 PPAHGVTSAPDTRPAP 20  
Db ||||| : : : : :  
27 PPAQGSSSSPRTPPAP 42  
  
RESULT 14  
Q95K74 PRELIMINARY; PRT; 282 AA.  
ID Q95K74;  
AC Q95K74;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
OC Cercopithecinae; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Temporal lobe right;  
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,  
RA Suzuki Y., Sugano S., Hashimoto K.;  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBSJ databases.  
DR EMBL; AB063097; BAB60803.1; -.  
KW Hypothetical protein.  
SQ SEQUENCE 282 AA; 30076 MW; 772F37069CE472C8 CRC64;  
  
Query Match 49.5%; Score 54; DB 2; Length 282;  
Best Local Similarity 62.5%; Pred. No. 36;  
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
  
QY 5 PPAHGVTSAPDTRPAP 20  
Db ||||| : : : : :  
27 PPAQGSSSSPRTPPAP 42  
  
RESULT 15

Q9N088  
ID Q9N088 PRELIMINARY; PRT; 282 AA.  
AC Q9N088;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)  
DE Unnamed protein product.  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecoidea; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21458551; PubMed=11574149; DOI=10.1016/S0378-1119(01)00665-5;  
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirata M., Suto Y.,  
RA Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K.;  
RT "Assignment of 118 novel cDNAs of cynomolgus monkey brain to human  
RT chromosomes.";  
RL Gene 275:31-37(2001).  
DR EMBL; AB046043; BAB01625.1; -.  
SQ SEQUENCE 282 AA; 30104 MW; A3C249DD8E62F6D5 CRC64;  
  
Query Match 49.5%; Score 54; DB 2; Length 282;  
Best Local Similarity 62.5%; Pred. No. 36;  
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
  
QY 5 PPAHGVTSPDTRPAP 20  
Db ||| | :|:| |  
27 PPAQGSSSPRTTPAP 42

Search completed: June 30, 2005, 06:50:02  
Job time : 348 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 30, 2005, 05:38:37 ; Search time 67 Seconds  
(without alignments)  
28.721 Million cell updates/sec

Title: US-10-057-136-1  
Perfect score: 109  
Sequence: 1 GSTAPPAHGVTSA PDTRPAP 20  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	109	100.0	1344	1	A35175	mucin 1 precursor,
2	104	95.4	347	2	S10571	mucin 1 precursor,
3	93	85.3	256	2	A60533	tumor-associated a
4	58.5	53.7	1334	2	T50568	probable multi-dom
5	52	47.7	244	2	AG0722	conserved hypothet
6	52	47.7	739	1	A34873	transcription fact
7	52	47.7	739	2	I56187	transcription fact
8	52	47.7	766	1	A47001	transcription fact
9	52	47.7	770	1	S30293	transcription fact
10	51	46.8	241	2	AC2284	hypothetical prote
11	51	46.8	377	2	T36246	probable glycolate
12	51	46.8	594	2	T12995	pectinesterase hom
13	50.5	46.3	648	2	T35120	hypothetical prote
14	50	45.9	330	2	T05717	probable extensin
15	49.5	45.4	576	2	T36729	probable serine/th
16	49	45.0	30	2	T30514	hypothetical prote
17	49	45.0	428	2	T24769	hypothetical prote
18	49	45.0	630	2	A39344	tumor-associated m
19	49	45.0	631	2	I52257	episialin - mouse
20	48	44.0	250	2	S71348	Rieske iron-sulfur
21	48	44.0	322	2	E90457	Rieske iron-sulfur
22	48	44.0	324	2	C90440	rieske iron-sulfur
23	48	44.0	551	2	F83015	hypothetical prote
24	48	44.0	691	2	A40024	regulatory protein
25	48	44.0	712	1	I46031	gelatinase B (EC 3
26	47	43.1	182	2	S73046	penicillin binding
27	47	43.1	411	2	D86995	probable D-alanyl-
28	47	43.1	526	2	T33047	hypothetical prote
29	47	43.1	544	2	A71260	hypothetical prote

30	47	43.1	633	2	E75277	ABC transporter, A
31	47	43.1	839	2	F75518	hypothetical prote
32	47	43.1	924	2	S75284	chemotaxis protein
33	46.5	42.7	418	2	T15142	hypothetical prote
34	46.5	42.7	459	1	P2WL6	L2 protein - human
35	46.5	42.7	668	1	QOBEW1	ULS2 protein - hum
36	46.5	42.7	897	2	E65127	Probable bifunctio
37	46	42.2	363	2	S44443	RAD23 protein homo
38	46	42.2	652	2	S71753	repellent protein
39	46	42.2	2187	2	T30826	nascent polypeptid
40	46	42.2	3345	2	T13423	hypothetical prote
41	45.5	41.7	168	2	T46341	hypothetical prote
42	45.5	41.7	245	2	AF3314	soluble lytic mure
43	45.5	41.7	314	2	D70927	probable lppW prot
44	45.5	41.7	2297	2	T34918	polyketide synthas
45	45.5	41.7	4135	2	T42629	tenascin-X - bovin

ALIGNMENTS

RESULT 1

A35175  
mucin 1 precursor, repetitive splice form A [validated] - human  
N;Alternate names: breast carcinoma-associated DF3 antigen; core protein KP39; episialin  
ncreatic mucin; polymorphic epithelial mucin (PEM)  
N;Contains: mucin 1 precursor, epithelial tumor antigen splice form; mucin 1 precursor,  
C;Species: Homo sapiens (man)  
C;Date: 20-Apr-2000 #sequence revision 20-Apr-2000 #text change 02-Jun-2000  
C;Accession: A35175; B35175; A35886; A35887; S10572; S40293; A36735; PX0066; S10218; S51  
R;Ligtenberg, M.J.L.; Vos, H.L.; Gennissen, A.M.C.; Hilkens, J.  
J. Biol. Chem. 265, 5573-5578, 1990  
A;Title: Episialin, a carcinoma-associated mucin, is generated by a polymorphic gene enc  
A;Reference number: A35175; MUID:90202794; PMID:2318825  
A;Accession: A35175  
A;Molecule type: mRNA  
A;Residues: 1-952,1033-1344 <LIG1>  
A;Cross-references: GB:M32738; GB:J05288; NID:gl82121; PIDN:AAA35804.1; PID:gl82124; GB:  
A;Experimental source: splice form A  
A;Note: GenBank entries HUMEPI5IA1 and HUMEPI5IA2 present only the amino-and carboxyl-en  
A;Accession: B35175  
A;Molecule type: mRNA  
A;Residues: 1-19,29-952,1033-1344 <LIG2>  
A;Cross-references: GB:M32739; GB:J05288; NID:gl82126; PIDN:AAA35806.1; PID:gl82129; GB:  
A;Experimental source: splice form B  
A;Note: GenBank entries HUMEPI5IB1 and HUMEPI5IB2 present only the amino-and carboxyl-en  
R;Gendler, S.J.; Lancaster, C.A.; Taylor-Papadimitriou, J.; Duhig, T.; Peat, N.; Burchel  
J. Biol. Chem. 265, 15286-15293, 1990  
A;Title: Molecular cloning and expression of human tumor-associated polymorphic epitheli  
A;Reference number: A35886; MUID:90368715; PMID:1697589  
A;Accession: A35886  
A;Status: not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-19,29-992,1033-1344 <GEN>  
A;Cross-references: GB:J05581; NID:gl88869; PIDN:AAA59876.1; PID:gl88870  
A;Note: GenBank entry HUMMUCAB includes one copy of the tandemly repeated sequence  
R;Lan, M.S.; Batra, S.K.; Qi, W.N.; Metzgar, R.S.; Hollingsworth, M.A.  
J. Biol. Chem. 265, 15294-15299, 1990  
A;Title: Cloning and sequencing of a human pancreatic tumor mucin cDNA.  
A;Reference number: A35887; MUID:90368716; PMID:2394722  
A;Accession: A35887  
A;Status: not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-19,29-1109,'S',1111-1339,'A',1341-1344 <LAN>  
A;Cross-references: GB:J05582; NID:gl89598; PIDN:AAA60019.1; PID:gl89599  
A;Note: GenBank entry HUMPANMU contains four fewer copies of the tandemly repeated seque  
R;Wreschner, D.H.; Hareuveni, M.; Tsarfaty, I.; Smorodinsky, N.; Horev, J.; Zaretsky, J.  
Eur. J. Biochem. 189, 463-473, 1990  
A;Title: Human epithelial tumor antigen cDNA sequences. Differential splicing may genera  
A;Reference number: S10571; MUID:90276413; PMID:2351132  
A;Accession: S10572  
A;Molecule type: mRNA  
A;Residues: 1-19,29-155,'P',157-175,'P',177-182,'A',184-212,1033-1344. <WRE>



A;Cross-references: EMBL:X52229; NID:g37053  
R;Wreschner, D.H.  
Submitted to the EMBL Data Library, March 1990  
A;Reference number: S40293  
A;Accession: S40293  
A;Molecule type: mRNA  
A;Residues: 1-19,29-155,'P',157-175,'P',177-182,'A',184-212,1033-1037,'A',1039-1344 <WR2  
A;Cross-references: EMBL:X52229; NID:g37053; PIDN:CAA36478.1; PID:g37054  
R;Abe, M.; Siddiqui, J.; Kufe, D.  
Biochem. Biophys. Res. Commun. 165, 644-649, 1989  
A;Title: Sequence analysis of the 5' region of the human DF3 breast carcinoma-associated  
A;Reference number: A36735; MUID:90088473; PMID:2597151  
A;Accession: A36735  
A;Molecule type: mRNA  
A;Residues: 1-142,'Q',144-162,'Q',164-168 <ABE>  
A;Cross-references: EMBL:M31823; NID:g181542; PIDN:AAA35757.1; PID:g181543  
R;Masuzawa, Y.; Miyauchi, T.; Hamanoue, M.; Ando, S.; Yoshida, J.; Takao, S.; Shimazu, H.  
J. Biochem. 112, 609-615, 1992  
A;Title: A novel core protein as well as polymorphic epithelial mucin carry peanut agglu  
A;Reference number: JX0235; MUID:93123189; PMID:1478919  
A;Accession: FX0066  
A;Molecule type: mRNA  
A;Residues: 998-1011,'ES',1014-1017;1018-1032,'T',1034-1037;1038-1057 <MAS>  
A;Experimental source: gastric carcinoma cell  
R;Zrihan-Licht, S.; Baruch, A.; Elroy-Stein, O.; Keydar, I.; Wreschner, D.H.  
FEBS Lett. 356, 130-136, 1994  
A;Title: Tyrosine phosphorylation of the MUC1 breast cancer membrane proteins cytokine  
A;Reference number: S51026; MUID:95080414; PMID:7988707  
A;Contents: annotation  
A;Note: undetermined tyrosine residues in the carboxyl-terminal non-repetitive region an  
C;Comment: This protein is length polymorphic. Individuals may have between 21 and 125 c  
partial repeats. The repeat shown is defined by SmaI nuclease sites.  
C;Comment: Serine and threonine residues in the tandem repeat domain are extensively gly  
C;Comment: For an alternative splice form without a tandem repeat domain, see PIR:S48146  
C;Genetics:  
A;Gene: GDB:MUC1; PUM  
A;Cross-references: GDB:120705; OMIM:158340  
A;Map position: lq21-lq23  
A;Introns: 20/1; 62/3; 1165/3; 1184/2; 1230/1; 1270/3; 1320/3  
C;Superfamily: polymorphic epithelial mucin  
C;Keywords: alternative splicing; duplication; glycoprotein; phosphoprotein; polymorphis  
F;1-1344/Product: mucin 1 precursor, splice form A #status predicted <PREA>  
F;1-62/Region: mucin 1 amino-terminal non-repetitive  
F;1-23/Domain: signal sequence #link PREA #status predicted <SIGA>  
F;1-19,29-32/Domain: signal sequence #link PREB #status predicted <SIGB>  
F;1-19,29-1344/Product: mucin 1 precursor, splice form B #status predicted <PREB>  
F;1-19,29-212,1033-1344/Product: mucin 1 precursor, epithelial tumor antigen splice form  
F;138-1017/Region: 20-residue repeats (GSTAPPAHGVTSA PDTRPAP)  
F;1143-1344/Region: mucin 1 carboxyl-terminal non-repetitive  
F;1245-1272/Domain: transmembrane #status predicted <TRM>  
F;1046,1064,1118,1144,1222/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;1213/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 100.0%; Score 109; DB 1; Length 1344;  
Best Local Similarity 100.0%; Pred. No. 7.7e-07;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSTAPPAHGVTSA PDTRPAP 20  
|||||  
Db 138 GSTAPPAHGVTSA PDTRPAP 157  
|||||

RESULT 2  
S10571  
mucin 1 precursor, secreted epithelial tumor antigen splice form - human  
N;Contains: mucin 1 secreted breast-cancer-associated splice form  
C;Species: Homo sapiens (man)  
C;Date: 07-Apr-1994 #sequence revision 07-Apr-1994 #text\_change 09-Jul-2004  
A;Accession: S10571; JN0100; I56024; S09706; S10217  
R;Wreschner, D.H.; Hareuveni, M.; Tsarfaty, I.; Smorodinsky, N.; Horev, J.; Zaretsky, J.  
Eur. J. Biochem. 189, 463-473, 1990  
A;Title: Human epithelial tumor antigen cDNA sequences. Differential splicing may genera  
A;Reference number: S10571; MUID:90276413; PMID:2351132

A;Accession: S10571  
A;Molecule type: mRNA  
A;Residues: 1-347 <WRE>  
A;Cross-references: UNIPROT:Q9UM18; EMBL:X52228; NID:g36434; PIDN:CAA36477.1; PID:g36435  
R;Tsarfaty, I.; Hareuveni, M.; Horev, J.; Zaretsky, J.; Weiss, M.; Jeltsch, J.M.; Garnie  
Gene 93, 313-318, 1990  
A;Title: Isolation and characterization of an expressed hypervariable gene coding for a  
A;Reference number: JN0100; MUID:91033045; PMID:1688329  
A;Accession: JN0100  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-135,'Q',137-142,'E',144-163,204-208,'A',210-347 <TSA>  
A;Cross-references: GB:M35093; NID:g182252; PIDN:AAB59612.1; PID:g182253  
R;Xing, P.X.; Tjandra, J.J.; Reynolds, K.; McLaughlin, P.J.; Purcell, D.F.J.; McKenzie,  
J. Immunol. 142, 3503-3509, 1989  
A;Title: Reactivity of anti-human milk fat globule antibodies with synthetic peptides.  
A;Reference number: I56024; MUID:89235154; PMID:2715633  
A;Accession: I56024  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 182-201 <RES>  
A;Cross-references: GB:M26316; NID:g516622; PIDN:AAA36336.1; PID:g516623  
R;Tendler, S.J.B.  
Biochem. J. 267, 733-737, 1990  
A;Title: Elements of secondary structure in a human epithelial mucin core peptide fragme  
A;Reference number: S09706; MUID:90253387; PMID:2339983  
A;Accession: S09706  
A;Molecule type: protein  
A;Residues: 182-201 <TEN>  
C;Genetics:  
A;Gene: GDB:MUC1; PUM  
A;Cross-references: GDB:120705; OMIM:158340  
A;Map position: lq21-lq23  
C;Keywords: alternative splicing; tandem repeat  
F;1-23/Domain: signal sequence #status predicted <SIG>  
F;1-24-347/Product: mucin 1, secreted epithelial tumor antigen splice form #status predict  
F;1-24-163,204-347/Product: mucin 1, secreted breast-cancer-associated splice form #status

Query Match 95.4%; Score 104; DB 2; Length 347;  
Best Local Similarity 95.0%; Pred. No. 9.2e-07;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GSTAPPAHGVTSA PDTRPAP 20  
|||||  
Db 129 GSTAPPAHGVTSA PDTRPPP 148  
|||||

RESULT 3  
A60533  
tumor-associated antigen DF3 - human  
C;Species: Homo sapiens (man)  
C;Date: 19-Mar-1993 #sequence\_revision 07-May-1993 #text\_change 09-Jul-2004  
C;Accession: A60533  
R;Merlo, G.R.; Siddiqui, J.; Cropp, C.S.; Liscia, D.S.; Lidereau, R.; Callahan, R.; Kufe  
Cancer Res. 49, 6966-6971, 1989  
A;Title: Frequent alteration of the DF3 tumor-associated antigen gene in primary human b  
A;Reference number: A60533; MUID:90058554; PMID:2582438  
A;Accession: A60533  
A;Status: not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-256 <MER>  
A;Cross-references: UNIPROT:Q7M4M7  
C;Genetics:  
A;Map position: lq21-q24  
C;Superfamily: proline-rich protein  
C;Keywords: glycoprotein; tandem repeat

Query Match 85.3%; Score 93; DB 2; Length 256;  
Best Local Similarity 85.0%; Pred. No. 2.1e-05;  
Matches 17; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GSTAPPAHGVTSA PDTRPAP 20  
|||||



Db 12 GSTAPPAHRVTSAPESRPAP 31

RESULT 4

T50568

probable multi-domain regulatory protein [imported] - Streptomyces coelicolor

C;Species: Streptomyces coelicolor

C;Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 09-Jul-2004

C;Accession: T50568

R;Redenbach, M.; Kieser, H.M.; Denapaita, D.; Eichner, A.; Cullum, J.; Kinashi, H.; Hopw Mol. Microbiol. 21, 77-96, 1996

A;Title: A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb s

A;Reference number: Z20556; MUID:97000351; PMID:8843436

A;Accession: T50568

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1334 <RED>

A;Cross-references: UNIPROT:Q9RKR9; EMBL:AL133220; PIDN:CAB61705.1

A;Experimental source: strain A3(2)

C;Genetics:

A;Note: SCC75A.05c

Query Match 53.7%; Score 58.5; DB 2; Length 1334;

Best Local Similarity 68.4%; Pred. No. 5.2;

Matches 13; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Qy 2 STAPPAHGVTSA PDTRPAP 20

Db 328 STAPP-HDTASADTAPAP 345

RESULT 5

AG0722

conserved hypothetical protein STY1926 [imported] - Salmonella enterica subsp. enterica

C;Species: Salmonella enterica subsp. enterica serovar Typhi

A;Note: this species has also been called Salmonella typhi

C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002

C;Accession: AG0722

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.

A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AG0722

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-244 <PAR>

A;Cross-references: GB:AL513382; PIDN:CAD05481.1; PID:g16502985; GSPDB:GN00176

C;Genetics:

A;Gene: STY1926

Query Match 47.7%; Score 52; DB 2; Length 244;

Best Local Similarity 69.2%; Pred. No. 7.1;

Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PPAHGVTSA PDTR 17

Db 125 PPYGVTTLPDR 137

RESULT 6

A34873

transcription factor Oct-1, octamer-binding - chicken

C;Species: Gallus gallus (chicken)

C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004

C;Accession: A34873

R;Petryniak, B.; Staudt, L.M.; Postema, C.E.; McCormack, W.T.; Thompson, C.B. Proc. Natl. Acad. Sci. U.S.A. 87, 1099-1103, 1990

A;Title: Characterization of chicken octamer-binding proteins demonstrates that POU doma

A;Reference number: A34873; MUID:90138945; PMID:1967834

A;Accession: A34873

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-739 <PET>

A;Cross-references: UNIPROT:P15143; GB:M29972; NID:g212466; PIDN:AAA48993.1; PID:g212467

C;Superfamily: transcription factor Oct-1; homeobox homology; POU domain homology

C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

F;281-348/Domain: POU domain homology <POU>

F;376-432/Domain: homeobox homology <HOX>

Query Match 47.7%; Score 52; DB 1; Length 739;

Best Local Similarity 47.4%; Pred. No. 22;

Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 2 STAPPAHGVTSA PDTRPAP 20

Db 506 STAPPASSAVTSPSLSPSP 524

RESULT 7

I56187

transcription factor Oct-1 - mouse (fragment)

C;Species: Mus sp. (mouse)

C;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 20-Aug-1999

C;Accession: I56187

R;Lerner, A.; D'Adamo, L.; Diener, A.C.; Clayton, L.K.; Reinherz, E.L. J. Immunol. 151, 3152-3162, 1993

A;Title: CD3 zeta/eta/theta locus is colinear with and transcribed antisense to the gene

A;Reference number: I56187; MUID:93389142; PMID:8376772

A;Accession: I56187

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-739 <RES>

A;Cross-references: GB:S65461; NID:g414379; PIDN:AAB28234.1; PID:g414380

C;Superfamily: transcription factor Oct-1; homeobox homology; POU domain homology

C;Keywords: DNA binding; homeobox; nucleus; transcription regulation

F;281-348/Domain: POU domain homology <POU>

F;376-432/Domain: homeobox homology <HOX>

Query Match 47.7%; Score 52; DB 2; Length 739;

Best Local Similarity 47.4%; Pred. No. 22;

Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 2 STAPPAHGVTSA PDTRPAP 20

Db 507 STAPPASSAVTSPSLSPSP 525

RESULT 8

A47001

transcription factor Oct-1 - human

C;Species: Homo sapiens (man)

C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 29-Sep-1999

C;Accession: A47001; A31754

R;Sturm, R.A.; Cassidy, J.L.; Das, G.; Romo, A.; Evans, G.A. Genomics 16, 333-341, 1993

A;Title: Chromosomal structure and expression of the human OTF1 locus encoding the oct-1

A;Reference number: A47001; MUID:93300505; PMID:8314572

A;Accession: A47001

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-766 <STU>

A;Note: the sequence in GenBank entry HSOC1, release 111.0, begins with Met-24

R;Sturm, R.A.; Das, G.; Herr, W. Genes Dev. 2, 1582-1599, 1988

A;Title: The ubiquitous octamer-binding protein Oct-1 contains a POU domain with a homeo

A;Reference number: A31754; MUID:89107993; PMID:2905684

A;Accession: A31754

A;Molecule type: mRNA

A;Residues: 'P', 8-400, 'R', 402-766 <ST2>

A;Cross-references: GB:X13403; NID:g35126; PIDN:CAA31767.1; PID:g35127

C;Genetics:

A;Gene: GDB:POU2F1; OTF1; OCT1

A;Cross-references: GDB:I20254; OMIM:164175

A;Map position: lq22-1q23  
C;Superfamily: transcription factor Oct-1; homeobox homology; POU domain homology  
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation  
F;310-377/Domain: POU domain homology <POU>  
F;403-459/Domain: homeobox homology <HOX>

Query Match 47.7%; Score 52; DB 1; Length 766;  
Best Local Similarity 47.4%; Pred. No. 22;  
Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 STAPPAHGVTSPADTRPAP 20  
||||| :|:|  
Db 533 STAPPASSAVTSPSLSPSP 551

RESULT 9  
S30293  
transcription factor Oct-1, splice form Oct-1A - mouse  
N;Alternate names: NF-A1; NF111; OBP100; OTF-1  
N;Contains: transcription factor Oct-1B  
C;Species: Mus musculus (house mouse)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: S30293; S30294; S30295; S31873; S31870; S09238; S53721; S53720; S22645; S26  
R;Suzuki, N.; Peter, W.; Ciesiolka, T.; Gruss, P.; Schoeler, H.R.  
Nucleic Acids Res. 21, 245-252, 1993  
A;Title: Mouse Oct-1 contains a composite homeodomain of human Oct-1 and Oct-2.  
A;Reference number: S30293; MUID:93181198; PMID:8441632  
A;Accession: S30293  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-770 <SU2>  
A;Cross-references: UNIPROT:P25425; EMBL:X68362; NID:g53465; PIDN:CAA48422.1; PID:g53466  
A;Accession: S30294  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-498,523-770 <SU2>  
A;Cross-references: EMBL:X68363; NID:g53471; PIDN:CAA48423.1; PID:g53472  
A;Accession: S30295  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-498,523-716,'DCFMDWRTF' <SU3>  
A;Cross-references: EMBL:X68364; NID:g53473; PIDN:CAA48424.1; PID:g53474  
A;Note: splice form Oct-1C  
R;Jaffe, J.; Hochberg, M.; Reich, L.; Ben-neriah, Y.; Bergman, Y.; Laskov, R.  
submitted to the EMBL Data Library, February 1993  
A;Description: Expression of different isoforms of murine oct-1 gene in various tissues.  
A;Reference number: S31870  
A;Accession: S31873  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 30-128,'P',130-607,'A',609-667,692-770 <JAF>  
A;Cross-references: EMBL:X70324; NID:g53467; PIDN:CAA49791.1; PID:g53468  
A;Accession: S31870  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 371-498,523-607,'A',609-770 <JA2>  
A;Cross-references: EMBL:X70325  
R;Goldsbrough, A.; Ashworth, A.; Willison, K.  
Nucleic Acids Res. 18, 1634, 1990  
A;Title: Cloning and sequencing of POU-boxes expressed in mouse testis.  
A;Reference number: S09237; MUID:90221898; PMID:1970171  
A;Accession: S09238  
A;Molecule type: DNA  
A;Residues: 305-367,'D',369-426 <GOL>  
A;Cross-references: EMBL:X51958; NID:g53475; PIDN:CAA36217.1; PID:g930193  
R;Jaffe, J.; Hochberg, M.; Riss, J.; Hasin, T.; Reich, L.; Laskov, R.  
Biochim. Biophys. Acta 1261, 201-209, 1995  
A;Title: Cloning, sequencing and expression of two isoforms of the murine oct-1 transcri  
A;Reference number: S53720; MUID:95226446; PMID:7711063  
A;Accession: S53721  
A;Status: preliminary; nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 30-128,'P',130-607,'A',609-667,692-770 <JA3>

A;Cross-references: EMBL:X70324; NID:g53467; PIDN:CAA49791.1; PID:g53468  
A;Accession: S53720  
A;Status: preliminary; nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 370-498,523-607,'A',609-770 <JA4>  
A;Cross-references: EMBL:X70325; NID:g53469; PIDN:CAA49792.1; PID:g53470  
R;Stepchenko, A.G.  
Nucleic Acids Res. 20, 1419, 1992  
A;Title: The nucleotide sequence of mouse OCT-1 cDNA.  
A;Reference number: S22645; MUID:92220620; PMID:1561098  
A;Accession: S22645  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 'MLDCSDCVLDSR',1-42,'L',44-53,72-498,523-607,'A',609-638 <STE>  
A;Cross-references: EMBL:X56230; NID:g53476; PIDN:CAA39679.1; PID:g53477  
C;Genetics:  
A;Gene: Oct-1  
A;Map position: 1  
C;Superfamily: transcription factor Oct-1; homeobox homology; POU domain homology  
C;Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regulati  
F;1-770/Product: transcription factor Oct-1A #status predicted <OC1A>  
F;1-498,523-770/Product: transcription factor Oct-1B #status predicted <OC1B>  
F;288-355/Domain: POU domain homology <POU>  
F;383-439/Domain: homeobox homology <HOX>

Query Match 47.7%; Score 52; DB 1; Length 770;  
Best Local Similarity 47.4%; Pred. No. 23;  
Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 STAPPAHGVTSPADTRPAP 20  
||||| :|:|  
Db 538 STAPPASSAVTSPSLSPSP 556

RESULT 10  
AC2284  
hypothetical protein all3826 [imported] - Nostoc sp. (strain PCC 7120)  
C;Species: Nostoc sp. PCC 7120  
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C;Accession: AC2284  
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi  
Nakazaki, N.; Shimpō, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
DNA Res. 8, 205-213, 2001  
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
A;Reference number: AB1807; MUID:21595285; PMID:11759840  
A;Accession: AC2284  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-241 <KUR>  
A;Cross-references: UNIPROT:Q8YQJ7; GB:BA000019; PIDN:BAH75525.1; PID:g17132960; GSPDB:G  
A;Experimental source: strain PCC 7120  
C;Genetics:  
A;Gene: all3826

Query Match 46.8%; Score 51; DB 2; Length 241;  
Best Local Similarity 61.1%; Pred. No. 9.5;  
Matches 11; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 TAPPAHGVTSPADTRPAP 20  
||||| :|:|  
Db 182 TAKPAASPTSKPTTSPAP 199

RESULT 11  
T36246  
probable glycolate oxidase - Streptomyces coelicolor  
C;Species: Streptomyces coelicolor  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C;Accession: T36246  
R;Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, March 1999  
A;Reference number: Z21602

```
A;Accession: T36246
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-377 <SAU>
A;Cross-references: UNIPROT:Q9Z4X8; EMBL:AL035640; PIDN:CAB38520.1; GSPDB:GN00070; SCOE
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOE:DB:SCE63.05
C;Superfamily: alpha-hydroxy acid dehydrogenase, FMN-dependent; (S)-2-hydroxy-acid oxida
F;2-296/Domain: (S)-2-hydroxy-acid oxidase homology <2HY>

Query Match          46.8%; Score 51; DB 2; Length 377;
Best Local Similarity 64.7%; Pred. No. 15;
Matches 11; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

QY 4 APPAHGVTSA PDTRPAP 20
||| ||| :|| |||
Db 356 APPHGPPTAP--RPAP 370

RESULT 12
T12995
pectinesterase homolog T21L8.150 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T12995
R;Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sa
submitted to the Protein Sequence Database, July 1999
A;Reference number: Z17586
A;Accession: T12995
A;Molecule type: DNA
A;Residues: 1-594 <CHO>
A;Cross-references: UNIPROT:Q9STY3; EMBL:AL096860; GSPDB:GN00061; ATSP:T21L8.150
A;Experimental source: cultivar Columbia; BAC clone T21L8
C;Genetics:
A;Gene: ATSP:T21L8.150
A;Map position: 3
A;Introns: 251/1; 363/1
C;Superfamily: pectinesterase

Query Match          46.8%; Score 51; DB 2; Length 594;
Best Local Similarity 45.5%; Pred. No. 24;
Matches 10; Conservative 4; Mismatches 6; Indels 2; Gaps 1;

QY 1 GSTAPPA--HGVTSA PDTRPAP 20
|: ||| | | : | : | : |
Db 31 GTDAPPWDHNVSPPTAPSP 52

RESULT 13
T35120
hypothetical protein SC4H2.21 SC4H2.21 - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T35120
R;Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, March 1998
A;Reference number: Z21568
A;Accession: T35120
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-648 <SEE>
A;Cross-references: UNIPROT:O69976; EMBL:AL022268; PIDN:CAA18348.1; GSPDB:GN00070; SCOE
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOE:DB:SC4H2.21
C;Superfamily: Escherichia coli plasmid ColV-K30 aerobactin biosynthesis protein iuca

Query Match          46.3%; Score 50.5; DB 2; Length 648;
Best Local Similarity 61.9%; Pred. No. 30;
Matches 13; Conservative 0; Mismatches 3; Indels 5; Gaps 2;

QY 3 TAP---PAHGVTSAPDTRPAP 20
```

```
Db 52 TAPRLAPAHGVLPGP--RPAP 70
||| ||| | |||
||| ||| | |||

RESULT 14
T05717
probable extensin - barley (fragment)
C;Species: Hordeum vulgare (barley)
C;Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 09-Jul-2004
C;Accession: T05717
R;Doan, D.N.P.; Sturaro, M.; Olsen, O.A.
submitted to the EMBL Data Library, July 1997
A;Description: Characterization of a nuclear cDNA encoding a probable extensin from dev
A;Reference number: Z15429
A;Accession: T05717
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-330 <DOA>
A;Cross-references: UNIPROT:O49870; EMBL:Z98204; PIDN:CAB10894.1
C;Genetics:
A;Gene: exi
A;Map position: 2
C;Superfamily: hydroxyproline-rich glycoprotein

Query Match          45.9%; Score 50; DB 2; Length 330;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 10; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 GSTAPPAHGVTSAPDTRPAP 20
||| ||| : | |||
Db 47 GSQAPPTYSPPTAKPTTPAP 66

RESULT 15
T36729
probable serine/threonine-specific protein kinase (EC 2.7.1.-) - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 16-Aug-2004
C;Accession: T36729
R;Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1999
A;Reference number: Z21612
A;Accession: T36729
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-576 <MUR>
A;Cross-references: UNIPROT:Q9XA04; EMBL:AL079308; PIDN:CAB45227.1; GSPDB:GN00070; SCOE
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOE:DB:SCH69.30
C;Superfamily: protein kinase homology
C;Keywords: phosphotransferase; serine/threonine-specific protein kinase

Query Match          45.4%; Score 49.5; DB 2; Length 576;
Best Local Similarity 56.0%; Pred. No. 37;
Matches 14; Conservative 0; Mismatches 6; Indels 5; Gaps 2;

QY 1 GSTAPP-AHGVTSAPD---TRPAP 20
| ||| | |||
Db 399 GPTAPPSAPSAPSAPSAPGPTRPAP 423

Search completed: June 30, 2005, 06:44:09
Job time : 68 secs
```

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 30, 2005, 06:29:25 ; Search time 1315 Seconds  
(without alignments)  
1.135 Million cell updates/sec

Title: US-10-057-136-1  
Perfect score: 109  
Sequence: 1 GSTAPPAHGVTSPDTRPAP 20

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCITUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	109	100.0	20	4 US-09-641-833-1	Sequence 1, Appli
2	109	100.0	30	3 US-08-737-896-6	Sequence 6, Appli
3	109	100.0	30	4 US-09-593-870A-47	Sequence 47, Appl
4	109	100.0	30	5 PCT-US96-09951-6	Sequence 6, Appli
5	109	100.0	32	4 US-09-593-870A-46	Sequence 46, Appl
6	109	100.0	40	1 US-08-099-354-1	Sequence 1, Appli
7	109	100.0	40	2 US-08-288-059-7	Sequence 7, Appli
8	103	94.5	25	4 US-09-497-232-5	Sequence 5, Appli
9	99	90.8	24	3 US-08-737-896-5	Sequence 5, Appli
10	99	90.8	24	4 US-09-497-232-23	Sequence 23, Appli
11	99	90.8	24	5 PCT-US96-09951-5	Sequence 5, Appli
12	99	90.8	25	4 US-09-217-306B-3	Sequence 3, Appli
13	98	89.9	30	3 US-08-134-198E-13	Sequence 13, Appli
14	95	87.2	177	4 US-09-646-028-54	Sequence 54, Appl
15	94	86.2	20	3 US-08-134-198E-35	Sequence 35, Appl
16	92	84.4	24	4 US-09-217-306B-16	Sequence 16, Appl
17	92	84.4	24	4 US-09-217-306B-17	Sequence 17, Appl
18	91	83.5	28	2 US-08-488-161-9	Sequence 9, Appli
19	91	83.5	28	3 US-09-273-685-9	Sequence 9, Appli
20	91	83.5	28	5 PCT-US95-11934-9	Sequence 9, Appli
21	91	83.5	1867	2 US-08-479-537A-5	Sequence 5, Appli
22	91	83.5	1867	3 US-09-083-116-5	Sequence 5, Appli
23	91	83.5	1867	3 US-09-134-916A-5	Sequence 5, Appli
24	91	83.5	2035	2 US-08-479-537A-2	Sequence 2, Appli
25	91	83.5	2035	3 US-09-083-116-2	Sequence 2, Appli
26	91	83.5	2035	3 US-09-134-916A-2	Sequence 2, Appli
27	90	82.6	172	4 US-09-646-028-49	Sequence 49, Appl

28	87	79.8	40	1	US-08-099-354-2	Sequence 2, Appli
29	87	79.8	40	2	US-08-288-059-8	Sequence 8, Appli
30	84	77.1	20	2	US-08-479-537A-3	Sequence 3, Appli
31	84	77.1	20	3	US-09-083-116-3	Sequence 3, Appli
32	84	77.1	20	3	US-09-134-916A-3	Sequence 3, Appli
33	83	76.1	20	2	US-08-833-807-8	Sequence 8, Appli
34	83	76.1	20	3	US-09-223-043-8	Sequence 8, Appli
35	83	76.1	20	3	US-09-291-351-1	Sequence 1, Appli
36	83	76.1	20	3	US-09-043-731-16	Sequence 16, Appl
37	83	76.1	20	4	US-09-593-870A-20	Sequence 20, Appl
38	83	76.1	21	2	US-08-833-807-7	Sequence 7, Appli
39	83	76.1	21	3	US-09-223-043-7	Sequence 7, Appli
40	83	76.1	21	3	US-09-043-731-15	Sequence 15, Appl
41	83	76.1	21	4	US-09-593-870A-19	Sequence 19, Appl
42	81	74.3	23	3	US-09-043-731-17	Sequence 17, Appl
43	77	70.6	134	4	US-09-646-028-1	Sequence 1, Appli
44	77	70.6	137	4	US-09-646-028-2	Sequence 2, Appli
45	77	70.6	138	4	US-09-646-028-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1  
US-09-641-833-1  
; Sequence 1, Application US/09641833  
; Patent No. 6716966  
; GENERAL INFORMATION:  
; APPLICANT: Madiyalakan, Ragupathy  
; TITLE OF INVENTION: Therapeutic Binding Agents Against MUC-1 Antigen and  
; TITLE OF INVENTION: Methods  
; TITLE OF INVENTION: for Their Use  
; FILE REFERENCE: 107823.127  
; CURRENT APPLICATION NUMBER: US/09/641,833  
; CURRENT FILING DATE: 2000-08-16  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: MUC-1 antigen  
US-09-641-833-1

Query Match 100.0%; Score 109; DB 4; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2e-08;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSTAPPAHGVTSPDTRPAP 20  
| | | | | | | | | | | | | | | | | |  
DB 1 GSTAPPAHGVTSPDTRPAP 20

RESULT 2  
US-08-737-896-6  
; Sequence 6, Application US/08737896  
; Patent No. 6168804  
; GENERAL INFORMATION:  
; APPLICANT: Samuel, John  
; APPLICANT: Kwon, Glen S.  
; TITLE OF INVENTION: METHOD FOR ELICITING TH1-SPECIFIC  
; TITLE OF INVENTION: IMMUNE RESPONSE  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette

```
;
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,896
; FILING DATE: 24-SEP-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/480,499
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: PCT/US96/09551
; FILING DATE: 07-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07254/037001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: SP1-070 MUC1
;
US-08-737-896-6
```

```
Query Match 100.0%; Score 109; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GSTAPPAHGVTSAPDTRPAP 20
Db 5 GSTAPPAHGVTSAPDTRPAP 24
```

```
RESULT 3
US-09-593-870A-47
; Sequence 47, Application US/09593870A
; Patent No. 6548643
; GENERAL INFORMATION:
; APPLICANT: McKenzie, Ian F.C.
; APPLICANT: Apostolopoulos, Vasso
; APPLICANT: Pietersz, Geoff Allan
; TITLE OF INVENTION: Antigen Carbohydrate Compounds and Their
; FILE REFERENCE: 2368-McKenzie
; CURRENT APPLICATION NUMBER: US/09/593,870A
; CURRENT FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: 09/223,043
; PRIOR FILING DATE: 1998-12-30
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 47
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-593-870A-47
```

```
Query Match 100.0%; Score 109; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GSTAPPAHGVTSAPDTRPAP 20
Db 8 GSTAPPAHGVTSAPDTRPAP 27
```

```
RESULT 4
PCT-US96-09951-6
; Sequence 6, Application PC/TUS9609951
; GENERAL INFORMATION:
```

```
;
; APPLICANT: The Governors of the University of Alberta
; TITLE OF INVENTION: A METHOD FOR ELICITING A THI-SPECIFIC
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: California
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09951
; FILING DATE: 06-JUN-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Learn, June M.
; REGISTRATION NUMBER: 31,238
; REFERENCE/DOCKET NUMBER: 07254/037W01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 678-5070
; TELEFAX: (619) 678-5099
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: SP1-070 MUC1
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..30
;
PCT-US96-09951-6
```

```
Query Match 100.0%; Score 109; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GSTAPPAHGVTSAPDTRPAP 20
Db 5 GSTAPPAHGVTSAPDTRPAP 24
```

```
RESULT 5
US-09-593-870A-46
; Sequence 46, Application US/09593870A
; Patent No. 6548643
; GENERAL INFORMATION:
; APPLICANT: McKenzie, Ian F.C.
; APPLICANT: Apostolopoulos, Vasso
; APPLICANT: Pietersz, Geoff Allan
; TITLE OF INVENTION: Antigen Carbohydrate Compounds and Their
; FILE REFERENCE: 2368-McKenzie
; CURRENT APPLICATION NUMBER: US/09/593,870A
; CURRENT FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: 09/223,043
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 46
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-593-870A-46
```

Query Match 100.0%; Score 109; DB 4; Length 32;  
Best Local Similarity 100.0%; Pred. No. 3.4e-08;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSTAPPAHGVTSPDTRPAP 20  
Db 8 GSTAPPAHGVTSPDTRPAP 27

RESULT 6  
US-08-099-354-1  
; Sequence 1, Application US/08099354  
; Patent No. 574144  
; GENERAL INFORMATION:  
; APPLICANT: FINN, OLIVERA J.  
; APPLICANT: FONTENOT, J. D.  
; APPLICANT: MONTELARO, RONALD C.  
; TITLE OF INVENTION: SYNTHETIC MULTIPLE TANDEM REPEAT MUCIN  
; TITLE OF INVENTION: AND MUCIN-LIKE PEPTIDES, AND USES THEREOF  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/099,354  
; FILING DATE: 30-JUL-1993  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SIRILLA, GEORGE M.  
; REGISTRATION NUMBER: 18221  
; REFERENCE/DOCKET NUMBER: 6137/202246  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-861-3536  
; TELEFAX: 202-822-0944  
; TELEX: 6714627 CUSH  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 40 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-099-354-1

Query Match 100.0%; Score 109; DB 1; Length 40;  
Best Local Similarity 100.0%; Pred. No. 4.3e-08;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSTAPPAHGVTSPDTRPAP 20  
Db 9 GSTAPPAHGVTSPDTRPAP 28

RESULT 7  
US-08-288-059-7  
; Sequence 7, Application US/08288059  
; Patent No. 5827666  
; GENERAL INFORMATION:  
; APPLICANT: FINN, OLIVERA J.  
; APPLICANT: FONTENOT, J. D.  
; APPLICANT: MONTELARO, RONALD C.  
; TITLE OF INVENTION: SYNTHETIC MULTIPLE TANDEM REPEAT MUCIN  
; TITLE OF INVENTION: AND MUCIN-LIKE PEPTIDES, AND USES THEREOF  
; NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/288,059  
FILING DATE: 08-AUG-1994  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: CHAPIN, MARLANA K.  
REGISTRATION NUMBER: 35,843  
REFERENCE/DOCKET NUMBER: 61137/205204  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3711  
TELEFAX: 202-822-0944  
TELEX: 6714627 CUSH  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-288-059-7

Query Match 100.0%; Score 109; DB 2; Length 40;  
Best Local Similarity 100.0%; Pred. No. 4.3e-08;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSTAPPAHGVTSPDTRPAP 20  
Db 9 GSTAPPAHGVTSPDTRPAP 28

RESULT 8  
US-09-497-232-5  
; Sequence 5, Application US/09497232  
; Patent No. 6600012  
; GENERAL INFORMATION:  
; APPLICANT: AGRAWAL, Babita  
; KRANTZ, Mark J.  
; REDDISH, Mark A.  
; LONGENECKER, B. Michael  
; TITLE OF INVENTION: METHOD FOR GENERATING ACTIVATED T-CELLS  
; AND ANTIGEN-PULSED ANTIGEN-PRESENTING CELLS  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY & LARDNER  
; STREET: 3000 K Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/497,232  
; FILING DATE: 03-Feb-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/074,410  
; FILING DATE: 08-MAY-1998



```

; APPLICATION NUMBER: US 60/045,949
; FILING DATE: 08-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 042881/0114
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-497-232-5

Query Match          94.5%; Score 103; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.6e-07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 STAPPAHGVTSAPDTRPAP 20
Db      1 STAPPAHGVTSAPDTRPAP 19

RESULT 9
US-08-737-896-5
; Sequence 5, Application US/08737896
; Patent No. 6168804
; GENERAL INFORMATION:
; APPLICANT: Samuel, John
; APPLICANT: Kwon, Glen S.
; TITLE OF INVENTION: METHOD FOR ELICITING TH1-SPECIFIC
; TITLE OF INVENTION: IMMUNE RESPONSE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,896
; FILING DATE: 24-SEP-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/480,499
; FILING DATE: 07-JUN-1996
; APPLICATION NUMBER: PCT/US96/09551
; FILING DATE: 07-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07254/037001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; CLONE: SPQ-065 MUC1

```

```

US-08-737-896-5

Query Match          90.8%; Score 99; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 TAPPAHGVTSAPDTRPAP 20
Db      1 TAPPAHGVTSAPDTRPAP 18

RESULT 10
US-09-497-232-23
; Sequence 23, Application US/09497232
; Patent No. 6600012
; GENERAL INFORMATION:
; APPLICANT: AGRAWAL, Babita
; KRANTZ, Mark J.
; REDDISH, Mark A.
; LONGENECKER, B. Michael
; TITLE OF INVENTION: METHOD FOR GENERATING ACTIVATED T-CELLS
; AND ANTIGEN-PULSED ANTIGEN-PRESENTING CELLS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/497,232
; FILING DATE: 03-Feb-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/074,410
; FILING DATE: 08-MAY-1998
; APPLICATION NUMBER: US 60/045,949
; FILING DATE: 08-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 042881/0114
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-497-232-23

Query Match          90.8%; Score 99; DB 4; Length 24;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 TAPPAHGVTSAPDTRPAP 20
Db      1 TAPPAHGVTSAPDTRPAP 18

RESULT 11
PCT-US96-09951-5
; Sequence 5, Application PC/TUS9609951

```



GENERAL INFORMATION:  
APPLICANT: The Governors of the University of Alberta  
TITLE OF INVENTION: A METHOD FOR ELICITING A Th1-SPECIFIC  
TITLE OF INVENTION: IMMUNE RESPONSE  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: California  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/09951  
FILING DATE: 06-JUN-1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: learn, June M.  
REGISTRATION NUMBER: 31,238  
REFERENCE/DOCKET NUMBER: 07254/037WO1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 678-5070  
TELEFAX: (619) 678-5099  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
CLONE: SPQ-065 MUC1  
FEATURE:  
NAME/KEY: Peptide  
LOCATION: 1..24  
PCT-US96-09951-5

Query Match 90.8%; Score 99; DB 5; Length 24;  
Best Local Similarity 100.0%; Pred. No. 5.4e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TAPPAHGVTSAPDTRPAP 20  
Db 1 TAPPAHGVTSAPDTRPAP 18

## RESULT 12

US-09-217-306B-3  
Sequence 3, Application US/09217306B  
Patent No. 6465220  
GENERAL INFORMATION:  
APPLICANT: Hassan, Helle  
APPLICANT: Clausen, Henrik  
APPLICANT: Bennett, Eric P.  
TITLE OF INVENTION: Glycosylation Using Galnac-T4 Transferase  
FILE REFERENCE: 8850\*1  
CURRENT APPLICATION NUMBER: US/09/217,306B  
CURRENT FILING DATE: 1998-12-21  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3  
LENGTH: 25  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: REPEAT  
LOCATION: (1)..(25)  
OTHER INFORMATION: MUC-1 tandem repeat

## US-09-217-306B-3

Query Match 90.8%; Score 99; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 5.7e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TAPPAHGVTSAPDTRPAP 20  
Db 1 TAPPAHGVTSAPDTRPAP 18

## RESULT 13

US-08-134-198E-13  
Sequence 13, Application US/08134198E  
Patent No. 6190885  
GENERAL INFORMATION:  
APPLICANT: CANCER RESEARCH FUND  
APPLICANT: OF CONTRA COSTA  
APPLICANT: PETERSON, JERRY A.  
APPLICANT: LARocca, DAVID J.  
TITLE OF INVENTION: FUSION PROTEIN CONTAINING HMFG  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder & Poplawski  
STREET: 444 South Flower Street, Suite 1900  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0,  
SOFTWARE: Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/134,198E  
FILING DATE: October 8, 1993  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Amzel, Viviana  
REGISTRATION NUMBER: 30,930  
REFERENCE/DOCKET NUMBER: P66 38208 (CRFC-003C)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 622-7700  
TELEFAX: (213) 489-4210  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 30  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-134-198E-13

Query Match 89.9%; Score 98; DB 3; Length 30;  
Best Local Similarity 100.0%; Pred. No. 9.4e-07;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSTAPPAHGVTSAPDTRP 18  
Db 13 GSTAPPAHGVTSAPDTRP 30

## RESULT 14

US-09-646-028-54  
Sequence 54, Application US/09646028  
Patent No. 6562347  
GENERAL INFORMATION:  
APPLICANT: Kwak, Larry  
APPLICANT: Biragyn, Arya  
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF  
TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES

FILE REFERENCE: 14014.0316/P  
CURRENT APPLICATION NUMBER: US/09/646,028  
CURRENT FILING DATE: 2000-09-12  
PRIOR APPLICATION NUMBER: 60/077,745  
PRIOR FILING DATE: 1998-03-12  
NUMBER OF SEQ ID NOS: 57  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 54  
LENGTH: 177  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct  
US-09-646-028-54

Query Match 87.2%; Score 95; DB 4; Length 177;  
Best Local Similarity 71.4%; Pred. No. 1.6e-05;  
Matches 20; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

OY 1 GSTAPPAH-----GVTSAPDTRPAP 20  
Db 116 GSTAPPAHGVTSAAALDGVTSAPDTRPAP 143

RESULT 15  
US-08-134-198E-35  
Sequence 35, Application US/08134198E  
Patent No. 6190885  
GENERAL INFORMATION:  
APPLICANT: CANCER RESEARCH FUND  
APPLICANT: OF CONTRA COSTA  
APPLICANT: PETERSON, JERRY A.  
APPLICANT: LARocca, DAVID J.  
TITLE OF INVENTION: FUSION PROTEIN CONTAINING HMF  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pretty, Schroeder & Poplawski  
STREET: 444 South Flower Street, Suite 1900  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0,  
SOFTWARE: Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/134,198E  
FILING DATE: October 8, 1993  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Amzel, Viviana  
REGISTRATION NUMBER: 30,930  
REFERENCE/DOCKET NUMBER: P66 38208 (CRFC-003C)  
TELEPHONE: (213) 622-7700  
TELEFAX: (213) 489-4210  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-134-198E-35

Query Match 86.2%; Score 94; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.1e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 APPAHGVTSAPDTRPAP 20

Db 1 APPAHGVTSAPDTRPAP 17  
Search completed: June 30, 2005, 07:12:01  
Job time : 1315 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 30, 2005, 06:39:50 ; Search time 349 Seconds  
(without alignments)  
22.109 Million cell updates/sec

Title: US-10-057-136-1

Perfect score: 109  
Sequence: 1 GSTAPPAHGVTSPDTRPAP 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1722976 seqs, 385795295 residues

Total number of hits satisfying chosen parameters: 1722976

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:  
1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US05\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US10E\_PUBCOMB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/2/pubpaa/US11A\_PUBCOMB.pep.\*  
20: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*  
21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	109	100.0	20	9	US-09-994-466-1
2	109	100.0	20	14	US-10-057-136-1
3	109	100.0	20	17	US-10-754-089-1
4	109	100.0	31	9	US-09-994-466-11
5	109	100.0	40	10	US-09-996-069-9
6	109	100.0	40	17	US-10-635-211-4
7	109	100.0	43	14	US-10-106-876-14
8	109	100.0	46	10	US-09-996-069-5
9	109	100.0	46	14	US-10-106-876-1
10	109	100.0	100	9	US-09-965-131-6
11	109	100.0	159	17	US-10-635-211-9

12	109	100.0	475	15	US-10-417-312-1	Sequence 1, Appli
13	109	100.0	475	17	US-10-696-639-59	Sequence 59, Appli
14	109	100.0	508	14	US-10-057-136-20	Sequence 20, Appli
15	109	100.0	586	17	US-10-635-211-2	Sequence 2, Appli
16	109	100.0	1255	10	US-09-996-069-10	Sequence 10, Appli
17	109	100.0	1255	14	US-10-171-311-158	Sequence 158, App
18	109	100.0	1255	14	US-10-177-293-311	Sequence 311, App
19	109	100.0	1255	16	US-10-734-564-120	Sequence 120, App
20	109	100.0	1255	17	US-10-473-484-2	Sequence 2, Appli
21	104	95.4	515	14	US-10-097-340-212	Sequence 212, App
22	104	95.4	515	14	US-10-171-311-156	Sequence 156, App
23	104	95.4	515	15	US-10-612-090-19	Sequence 19, Appli
24	103	94.5	26	9	US-09-815-346-5	Sequence 5, Appli
25	103	94.5	26	14	US-10-106-876-8	Sequence 8, Appli
26	103	94.5	27	9	US-09-870-691-1	Sequence 1, Appli
27	103	94.5	27	9	US-09-999-191-1	Sequence 1, Appli
28	103	94.5	27	14	US-10-106-876-12	Sequence 12, Appli
29	103	94.5	28	14	US-10-106-876-13	Sequence 13, Appli
30	100	91.7	20	14	US-10-057-136-16	Sequence 16, Appli
31	99	90.8	20	9	US-09-984-333-9	Sequence 9, Appli
32	99	90.8	24	14	US-10-292-896-2	Sequence 2, Appli
33	99	90.8	24	17	US-10-705-401-2	Sequence 2, Appli
34	99	90.8	25	10	US-09-881-339-3	Sequence 3, Appli
35	99	90.8	25	15	US-10-417-633-3	Sequence 3, Appli
36	99	90.8	27	9	US-09-815-346-4	Sequence 4, Appli
37	99	90.8	27	14	US-10-106-876-7	Sequence 7, Appli
38	99	90.8	27	14	US-10-106-876-9	Sequence 9, Appli
39	98.5	90.4	35	16	US-10-471-607-15	Sequence 15, Appli
40	98.5	90.4	49	16	US-10-471-607-14	Sequence 14, Appli
41	98.5	90.4	49	16	US-10-471-607-16	Sequence 16, Appli
42	97	89.0	20	14	US-10-057-136-17	Sequence 17, Appli
43	95	87.2	26	14	US-10-106-876-20	Sequence 20, Appli
44	95	87.2	177	14	US-10-335-394-54	Sequence 54, Appli
45	94	86.2	25	14	US-10-292-896-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1  
US-09-994-466-1  
; Sequence 1, Application US/09994466  
; Publication No. US20020132771A1  
; GENERAL INFORMATION:  
; APPLICANT: Madiyalakan, R.  
; TITLE OF INVENTION: THERAPEUTIC BINDING AGENTS AGAINST MUC-1 ANTIGEN AND METHODS FOR  
; FILE REFERENCE: AREX-P03-002  
; CURRENT APPLICATION NUMBER: US/09/994,466  
; CURRENT FILING DATE: 2001-11-26  
; PRIOR APPLICATION NUMBER: 09/724094  
; PRIOR FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 20  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-994-466-1

Query Match 100.0%; Score 109; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.3e-07;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSTAPPAHGVTSPDTRPAP 20  
|||||  
Db 1 GSTAPPAHGVTSPDTRPAP 20

RESULT 2  
US-10-057-136-1  
; Sequence 1, Application US/10057136  
; Publication No. US20030021770A1

```

; GENERAL INFORMATION:
; APPLICANT: SCHLOM, JEFFREY
; APPLICANT: KANTOR, JUDITH
; APPLICANT: KUFE, DONALD
; APPLICANT: PANICALI, DENNIS
; APPLICANT: GRITZ, LINDA
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1
; FILE REFERENCE: 700953/47113C
; CURRENT APPLICATION NUMBER: US/10/057,136
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 09/366,670
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: PCT/US98/03693
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 60/038,253
; PRIOR FILING DATE: 1997-02-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-057-136-1

Query Match      100.0%; Score 109; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSTAPPAHGVTSAPDTRPAP 20
Db 1 GSTAPPAHGVTSAPDTRPAP 20

RESULT 3
US-10-754-089-1
; Sequence 1, Application US/10754089
; Publication No. US20050048059A1
; GENERAL INFORMATION:
; APPLICANT: Madiyalakan, Ragupathy
; TITLE OF INVENTION: Therapeutic Binding Agents Against MUC-1 Antigen and
; TITLE OF INVENTION: Methods
; TITLE OF INVENTION: for Their Use
; FILE REFERENCE: 107823.127
; CURRENT APPLICATION NUMBER: US/10/754,089
; CURRENT FILING DATE: 2004-01-07
; PRIOR APPLICATION NUMBER: US/09/641,833
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MUC-1 antigen
; US-10-754-089-1

Query Match      100.0%; Score 109; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSTAPPAHGVTSAPDTRPAP 20
Db 1 GSTAPPAHGVTSAPDTRPAP 20

RESULT 4
US-09-994-466-11
; Sequence 11, Application US/09994466
; Publication No. US20020132771A1
; GENERAL INFORMATION:
; APPLICANT: Madiyalakan, R.

```

```

; TITLE OF INVENTION: THERAPEUTIC BINDING AGENTS AGAINST MUC-1 ANTIGEN AND METHODS FOR
; TITLE OF INVENTION: THEIR USE
; FILE REFERENCE: AREX-P03-002
; CURRENT APPLICATION NUMBER: US/09/994,466
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 09/724094
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-994-466-11

Query Match      100.0%; Score 109; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSTAPPAHGVTSAPDTRPAP 20
Db 9 GSTAPPAHGVTSAPDTRPAP 28

RESULT 5
US-09-996-069-9
; Sequence 9, Application US/09996069
; Publication No. US20030036199A1
; GENERAL INFORMATION:
; APPLICANT: Bamdad, Cynthia
; APPLICANT: Bamdad, R. Shoshana
; TITLE OF INVENTION: DIAGNOSTIC TUMOR MARKERS, DRUG SCREENING FOR TUMORIGENESIS INHIBI
; TITLE OF INVENTION: AND COMPOSITIONS AND METHODS FOR TREATMENT OF CANCER
; FILE REFERENCE: M01015/70071
; CURRENT APPLICATION NUMBER: US/09/996,069
; CURRENT FILING DATE: 2001-11-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-996-069-9

Query Match      100.0%; Score 109; DB 10; Length 40;
Best Local Similarity 100.0%; Pred. No. 4.6e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSTAPPAHGVTSAPDTRPAP 20
Db 8 GSTAPPAHGVTSAPDTRPAP 27

RESULT 6
US-10-635-211-4
; Sequence 4, Application US/10635211
; Publication No. US20050031649A1
; GENERAL INFORMATION:
; APPLICANT: Beijing HYDVAX Biotechnology Co. Ltd
; TITLE OF INVENTION: A recombinant fusion protein comprising BCG heat shock protein 65
; TITLE OF INVENTION: and the epitope of MUC1
; FILE REFERENCE: FP03012US
; CURRENT APPLICATION NUMBER: US/10/635,211
; CURRENT FILING DATE: 2003-08-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-635-211-4

Query Match      100.0%; Score 109; DB 17; Length 40;

```

```
Best Local Similarity 100.0%; Pred. No. 4.6e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSTAPPAHGVTSAPDTRPAP 20
   |||||
Db 1 GSTAPPAHGVTSAPDTRPAP 20

RESULT 7
US-10-106-876-14
; Sequence 14, Application US/10106876
; Publication No. US20030157160A1
; GENERAL INFORMATION:
; APPLICANT: BUDZYNSKI, WLADYSLAW A.
; APPLICANT: KOGANTY, R. RAO
; APPLICANT: KRANTZ, MARK J.
; APPLICANT: LONGENECKER, B. MICHAEL
; TITLE OF INVENTION: VACCINE FOR MODULATING BETWEEN T1 AND T2 IMMUNE
; TITLE OF INVENTION: RESPONSES
; FILE REFERENCE: 042881-0176
; CURRENT APPLICATION NUMBER: US/10/106,876
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 60/278,698
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-106-876-14

Query Match 100.0%; Score 109; DB 14; Length 43;
Best Local Similarity 100.0%; Pred. No. 5e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSTAPPAHGVTSAPDTRPAP 20
   |||||
Db 11 GSTAPPAHGVTSAPDTRPAP 30

RESULT 8
US-09-996-069-5
; Sequence 5, Application US/09996069
; Publication No. US20030036199A1
; GENERAL INFORMATION:
; APPLICANT: Bamdad, Cynthia
; APPLICANT: Bamdad, R. Shoshana
; TITLE OF INVENTION: DIAGNOSTIC TUMOR MARKERS, DRUG SCREENING FOR TUMORIGENESIS INHIBI
; TITLE OF INVENTION: AND COMPOSITIONS AND METHODS FOR TREATMENT OF CANCER
; FILE REFERENCE: M01015/70071
; CURRENT APPLICATION NUMBER: US/09/996,069
; CURRENT FILING DATE: 2001-11-27
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-069-5

Query Match 100.0%; Score 109; DB 10; Length 46;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSTAPPAHGVTSAPDTRPAP 20
   |||||
Db 8 GSTAPPAHGVTSAPDTRPAP 27
```

```
RESULT 9
US-10-106-876-1
; Sequence 1, Application US/10106876
; Publication No. US20030157160A1
; GENERAL INFORMATION:
; APPLICANT: BUDZYNSKI, WLADYSLAW A.
; APPLICANT: KOGANTY, R. RAO
; APPLICANT: KRANTZ, MARK J.
; APPLICANT: LONGENECKER, B. MICHAEL
; TITLE OF INVENTION: VACCINE FOR MODULATING BETWEEN T1 AND T2 IMMUNE
; TITLE OF INVENTION: RESPONSES
; FILE REFERENCE: 042881-0176
; CURRENT APPLICATION NUMBER: US/10/106,876
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 60/278,698
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-106-876-1

Query Match 100.0%; Score 109; DB 14; Length 46;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSTAPPAHGVTSAPDTRPAP 20
   |||||
Db 14 GSTAPPAHGVTSAPDTRPAP 33

RESULT 10
US-09-965-131-6
; Sequence 6, Application US/09965131
; Patent No. US20020160502A1
; GENERAL INFORMATION:
; APPLICANT: Chung, Maureen A.
; APPLICANT: Sharma, Surendra
; APPLICANT: Chang, Helena R.
; APPLICANT: O'Donnell, Mark A.
; TITLE OF INVENTION: RECOMBINANT BCG VACCINES FOR THE
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF CANCER
; FILE REFERENCE: WII-014CP
; CURRENT APPLICATION NUMBER: US/09/965,131
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/235,455
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-965-131-6

Query Match 100.0%; Score 109; DB 9; Length 100;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSTAPPAHGVTSAPDTRPAP 20
   |||||
Db 13 GSTAPPAHGVTSAPDTRPAP 32

RESULT 11
US-10-635-211-9
; Sequence 9, Application US/10635211
; Publication No. US20050031649A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Beijing HYDVAX Biotechnology Co. Ltd
; TITLE OF INVENTION: A recombinant fusion protein comprising BCG heat shock protein 65
; TITLE OF INVENTION: and the epitope of MUC1
; FILE REFERENCE: FP03012US
; CURRENT APPLICATION NUMBER: US/10/635,211
; CURRENT FILING DATE: 2003-08-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 159
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion Protein
US-10-635-211-9

Query Match      100.0%; Score 109; DB 17; Length 159;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GSTAPPAHGVTSAPDTRPAP 20
Db      14 GSTAPPAHGVTSAPDTRPAP 33

RESULT 12
US-10-417-312-1
; Sequence 1, Application US/10417312
; Publication No. US20030235868A1
; GENERAL INFORMATION:
; APPLICANT: Dyax Corp
; TITLE OF INVENTION: Antibodies Specific for Mucin Polypeptide
; FILE REFERENCE: 2403/2002
; CURRENT APPLICATION NUMBER: US/10/417,312
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: US 60/374,432
; PRIOR FILING DATE: 2002-04-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-417-312-1

Query Match      100.0%; Score 109; DB 15; Length 475;
Best Local Similarity 100.0%; Pred. No. 5.9e-06;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GSTAPPAHGVTSAPDTRPAP 20
Db      129 GSTAPPAHGVTSAPDTRPAP 148

RESULT 13
US-10-696-639-59
; Sequence 59, Application US/10696639
; Publication No. US20050037439A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corporation
; APPLICANT: Bournier, Maureen J.
; TITLE OF INVENTION: DIFFERENTIALLY EXPRESSED GENES INVOLVED IN CANCER, THE
; TITLE OF INVENTION: POLYPEPTIDES ENCODED THEREBY, AND METHODS OF USING THE SAME
; FILE REFERENCE: 01040/1
; CURRENT APPLICATION NUMBER: US/10/696,639
; CURRENT FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/422,176
; PRIOR FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 3114
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 475

```

```

; TYPE: PRT
; ORGANISM: homo sapiens
US-10-696-639-59

Query Match      100.0%; Score 109; DB 17; Length 475;
Best Local Similarity 100.0%; Pred. No. 5.9e-06;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GSTAPPAHGVTSAPDTRPAP 20
Db      129 GSTAPPAHGVTSAPDTRPAP 148

RESULT 14
US-10-057-136-20
; Sequence 20, Application US/10057136
; Publication No. US20030021770A1
; GENERAL INFORMATION:
; APPLICANT: SCHLOM, JEFFREY
; APPLICANT: KANTOR, JUDITH
; APPLICANT: KUFU, DONALD
; APPLICANT: PANICALI, DENNIS
; APPLICANT: GRITZ, LINDA
; TITLE OF INVENTION: RECOMBINANT POX VIRUS FOR IMMUNIZATION AGAINST MUC1
; FILE REFERENCE: 700953/47113C
; CURRENT APPLICATION NUMBER: US/10/057,136
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 09/366,670
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: PCT/US98/03693
; PRIOR FILING DATE: 1998-02-24
; PRIOR APPLICATION NUMBER: 60/038,253
; PRIOR FILING DATE: 1997-02-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-057-136-20

Query Match      100.0%; Score 109; DB 14; Length 508;
Best Local Similarity 100.0%; Pred. No. 6.4e-06;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GSTAPPAHGVTSAPDTRPAP 20
Db      76 GSTAPPAHGVTSAPDTRPAP 95

RESULT 15
US-10-635-211-2
; Sequence 2, Application US/10635211
; Publication No. US20050031649A1
; GENERAL INFORMATION:
; APPLICANT: Beijing HYDVAX Biotechnology Co. Ltd
; TITLE OF INVENTION: A recombinant fusion protein comprising BCG heat shock protein 65
; TITLE OF INVENTION: and the epitope of MUC1
; FILE REFERENCE: FP03012US
; CURRENT APPLICATION NUMBER: US/10/635,211
; CURRENT FILING DATE: 2003-08-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant gene
US-10-635-211-2

Query Match      100.0%; Score 109; DB 17; Length 586;

```

Best Local Similarity 100.0%; Pred. No. 7.4e-06;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GSTAPPAGVTSAPDTRPAP 20  
Db 547 GSTAPPAGVTSAPDTRPAP 566

Search completed: June 30, 2005, 07:17:59  
Job time : 350 secs



**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 30, 2005, 05:30:29 ; Search time 288 Seconds  
(without alignments)  
26.858 Million cell updates/sec

Title: US-10-057-136-1

Perfect score: 109

Sequence: 1 GSTAPPAHGVTSPDTRPAP 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	109	100.0	20	AAW77229	Peptide s
2	109	100.0	20	ADL15164	Adl15164 Human tum
3	109	100.0	20	ADN00795	Adn00795 Human muc
4	109	100.0	26	AAW77230	Peptide s
5	109	100.0	27	ADN00796	Adn00796 Human muc
6	109	100.0	28	AAW03362	AAW03362 Mucin tan
7	109	100.0	30	AAW35737	AAW35737 Mucin pep
8	109	100.0	30	AAW01781	AAW01781 Synthetic
9	109	100.0	30	AAE09543	AAE09543 Human muc
10	109	100.0	31	AAW31695	AAW31695 Mucin pep
11	109	100.0	31	ABG73816	Abg73816 Tumour-ab
12	109	100.0	32	AAE09541	AAE09541 Human muc
13	109	100.0	40	AAR68002	Aar68002 Mucin rep
14	109	100.0	40	AAW54873	AAW54873 Carcinoma
15	109	100.0	40	AAW72703	AAW72703 Human muc
16	109	100.0	40	ABP56039	Abp56039 Repeat mo
17	109	100.0	40	ADF32639	Adf32639 MUC-1 rel
18	109	100.0	41	AAAY96170	AAAY96170 MUC1 repe
19	109	100.0	43	AAE33952	AAE33952 Dilipidat
20	109	100.0	43	ADD88870	Add88870 Synthetic
21	109	100.0	46	ABP56035	Abp56035 Histidine
22	109	100.0	46	AAE33936	AAE33936 MUC 1 pep
23	109	100.0	50	AAW35739	AAW35739 Mucin pep
24	109	100.0	51	AAW31697	AAW31697 Mucin pep
25	109	100.0	100	ABB76181	Abb76181 Synthetic

26	109	100.0	105	2	AAR68022	Aar68022 Mucin pep
27	109	100.0	105	2	AAW72697	Aaw72697 Synthetic
28	109	100.0	173	3	AAAY71021	Aay71021 Human Muc
29	109	100.0	216	3	AAAY92665	Aay92665 MUC-1 ana
30	109	100.0	295	3	AAAY71027	Aay71027 Ubiquitin
31	109	100.0	316	8	ADIS7755	Adi57755 Human bre
32	109	100.0	325	8	ADIS7777	Adi57777 Human bre
33	109	100.0	336	8	ADIS7782	Adi57782 Human bre
34	109	100.0	350	8	ADIS7754	Adi57754 Human bre
35	109	100.0	372	8	ADIS7758	Adi57758 Human bre
36	109	100.0	379	8	ADIS7779	Adi57779 Human bre
37	109	100.0	396	8	ADIS7776	Adi57776 Human bre
38	109	100.0	398	8	ADIS7765	Adi57765 Human bre
39	109	100.0	409	8	ADIS7778	Adi57778 Human bre
40	109	100.0	420	8	ADIS7770	Adi57770 Human bre
41	109	100.0	455	3	AAAY71024	Aay71024 Human Muc
42	109	100.0	463	8	ADIS7750	Adi57750 Human bre
43	109	100.0	473	4	AAE09508	Aae09508 Human muc
44	109	100.0	475	4	AAU00573	Aau00573 Human MUC
45	109	100.0	475	5	ABB77476	Abb77476 Human MUC

ALIGNMENTS

RESULT 1  
AAW77229  
ID AAW77229 standard; peptide; 20 AA.  
XX  
AC AAW77229;  
XX  
DT 20-NOV-1998 (first entry)  
XX  
DE Peptide sequence encoding MUC1 tandem repeat unit.  
XX  
KW MUC1; recombinant pox virus; cytotoxic T-lymphocyte; immunogen; tumour;  
KW tumour-associated antigen.  
XX  
OS Homo sapiens.  
XX  
PN WO9837095-A2.  
XX  
PD 27-AUG-1998.  
XX  
PF 24-FEB-1998; 98WO-US003693.  
XX  
PR 24-FEB-1997; 97US-0038253P.  
XX  
(THER-) THERION BIOLOGICS CORP.  
(USSH ) US DEPT HEALTH & HUMAN SERVICES.  
(DAND ) DANA FARBER CANCER INST INC.  
Schlom J, Kantor J, Kufe D, Panicali D, Gritz L;  
WPI; 1998-467492/40.  
N-PSDB; AAV48316.  
New recombinant pox virus for tumour therapy - comprises DNA encoding an immunogenic mini-MUC1 fragment comprising 5-25 MUC1 tandem repeat units.  
Example 1; Page 20; 42pp; English.  
The MUC1 tandem repeat unit was used to create an immunogenic mini-MUC1 fragment for inclusion in a recombinant pox virus (RPV). The RPV was used in a pharmaceutical composition also containing an immunomodulator to generate MUC1 specific cytotoxic T-lymphocytes. The recombinant pox virus therefore encodes an immunogenic MUC1 fragment that does not undergo significant genetic deletion, thereby providing an unexpectedly stable and immunogenic pox virus. They can be used to prevent or treat tumours expressing MUC1 tumour-associated antigens  
Sequence 20 AA;

Query Match 100.0%; Score 109; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-07;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSTAPPAHGVTSAPDTRPAP 20  
 |||||  
 Db 1 GSTAPPAHGVTSAPDTRPAP 20  
 |||||

RESULT 2  
 ADL15164  
 ID ADL15164 standard; peptide; 20 AA.  
 XX  
 AC ADL15164;  
 XX  
 DT 17-JUN-2004 (first entry)  
 XX  
 DE Human tumour-associated antigen, MUC-1 peptide #1.  
 XX  
 KW Therapeutic binding agent; tumour-associated antigen; MUC-1; cancer;  
 KW tumour; breast carcinoma; colon carcinoma;  
 KW oesophageal squamous cell carcinoma; pancreatic carcinoma;  
 KW prostate carcinoma; multiple myeloma; cytostatic; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6716966-B1.  
 XX  
 PD 06-APR-2004.  
 XX  
 PF 18-AUG-2000; 2000US-00641833.  
 XX  
 PR 18-AUG-1999; 99US-0149492P.  
 PR 11-NOV-1999; 99US-0164714P.  
 XX  
 PA (ALTA-) ALTAREX CORP.  
 XX  
 PI Madiyalakan R;  
 XX  
 DR WPI; 2004-303095/28.  
 XX  
 PT New binding agent, Alt-1, that binds immunological determinants of MUC-1,  
 PT useful for therapeutically treating a mammal bearing a tumor e.g. breast,  
 PT colon, esophageal, prostate or pancreatic carcinoma, or multiple myeloma.  
 XX  
 PS Disclosure; SEQ ID NO 1; 18pp; English.  
 XX  
 CC The present invention relates to therapeutic binding agents that bind to  
 CC tumour-associated antigen, MUC-1. The binding agent reduces, reverses, or  
 CC prevents the effects of MUC-1 in cancer. The binding agent is useful for  
 CC treating a mammal bearing a tumour e.g. breast carcinoma, colon  
 CC carcinoma, oesophageal squamous cell carcinoma, pancreatic carcinoma,  
 CC prostate carcinoma or multiple myeloma. The present sequence represents a  
 CC human MUC-1 peptide.  
 XX  
 SQ Sequence 20 AA;

Query Match 100.0%; Score 109; DB 8; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-07;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSTAPPAHGVTSAPDTRPAP 20  
 |||||  
 Db 1 GSTAPPAHGVTSAPDTRPAP 20  
 |||||

RESULT 3  
 ADN00795  
 ID ADN00795 standard; peptide; 20 AA.  
 XX  
 AC ADN00795;  
 XX  
 DT 15-JUL-2004 (first entry)

XX Human mucin 1 (MUC-1) peptide SeqID2.  
 DE  
 XX  
 KW cell-specific antigen; peripheral blood mononuclear cell;  
 KW immunogenic epitope; T lymphocyte; antigen-specific activation;  
 KW tumour-specific antigen; human mucin 1; MUC-1; cytostatic;  
 KW immunosuppressive; antimicrobial; tumour; adenocarcinomas; HIV infection;  
 KW autoimmune disease; infectious disease; human.  
 XX  
 OS Homo sapiens.  
 PN WO2004033667-A2.  
 XX  
 PD 22-APR-2004.  
 XX  
 PF 10-OCT-2003; 2003WO-US032602.  
 XX  
 PR 10-OCT-2002; 2002US-0417303P.  
 XX  
 PA (USGO ) US DEPT VETERANS AFFAIRS.  
 XX  
 PI Phillips CA;  
 XX  
 DR WPI; 2004-340926/31.  
 XX  
 PT Detecting and localizing a cell-specific antigen, useful in diagnosing  
 PT and treating e.g. tumors, HIV infection, autoimmune disease or infectious  
 PT disease, comprises exposing the peripheral blood mononuclear cells to an  
 PT immunogenic epitope.  
 XX  
 PS Claim 19; SEQ ID NO 2; 61pp; English.  
 XX  
 CC This invention relates to a novel method of detecting and localising a  
 CC cell-specific antigen in a mammal which comprises exposing the peripheral  
 CC blood mononuclear cells to a peptide that displays an immunogenic epitope  
 CC of the cell-specific antigen under conditions such that T lymphocytes in  
 CC the peripheral blood mononuclear cells undergo antigen-specific  
 CC activation, thus producing antigen-specific T lymphocytes that bind to  
 CC the cell-specific antigen. The cell-specific antigen is preferably a  
 CC tumour-specific antigen and the peptide displays an epitope of human  
 CC mucin 1 (MUC-1). The invention may be useful for the development of  
 CC compounds with a cytostatic, immunosuppressive or antimicrobial activity.  
 CC The method is useful in detecting and localising a cell-specific antigen  
 CC in a mammal. The method is useful in diagnosing and treating tumours,  
 CC particularly adenocarcinomas, HIV infection, autoimmune disease or  
 CC infectious disease and in monitoring response to therapy. The present  
 CC sequence is that of a human mucin 1 (MUC-1) epitope peptide which may be  
 CC used in the method of the invention.  
 XX  
 SQ Sequence 20 AA;

Query Match 100.0%; Score 109; DB 8; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-07;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSTAPPAHGVTSAPDTRPAP 20  
 |||||  
 Db 1 GSTAPPAHGVTSAPDTRPAP 20  
 |||||

RESULT 4  
 AAW77230  
 ID AAW77230 standard; peptide; 26 AA.  
 XX  
 AC AAW77230;  
 XX  
 DT 20-NOV-1998 (first entry)  
 XX  
 DE Peptide sequence encoding MUC1 tandem repeat unit a.  
 DE  
 KW MUC1; recombinant pox virus; cytotoxic T-lymphocyte; immunogen; tumour;  
 KW tumour-associated antigen.  
 XX

OS Homo sapiens.  
 PN WO9837095-A2.  
 XX  
 PD 27-AUG-1998.  
 XX  
 PF 24-FEB-1998; 98WO-US003693.  
 XX  
 PR 24-FEB-1997; 97US-0038253P.  
 XX  
 PA (THER-) THERION BIOLOGICS CORP.  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA (DAND ) DANA FARBER CANCER INST INC.  
 XX  
 PI Schlom J, Kantor J, Kufe D, Panicali D, Gritz L;  
 XX  
 DR WPI; 1998-467492/40.  
 DR N-PSDB; AAV48326.  
 XX  
 PT New recombinant pox virus for tumour therapy - comprises DNA encoding an  
 PT immunogenic mini-MUC1 fragment comprising 5-25 MUC1 tandem repeat units.  
 XX  
 PS Example 1; Page 20; 42pp; English.  
 XX  
 CC The MUC1 tandem repeat units AAW77230-W77232 were used to create an  
 CC immunogenic mini-MUC1 fragment for inclusion in a recombinant pox virus  
 CC (RPV). The RPV was used in a pharmaceutical composition also containing  
 CC an immunomodulator to generate MUC1 specific cytotoxic T-lymphocytes. The  
 CC recombinant pox virus therefore encodes an immunogenic MUC1 fragment that  
 CC does not undergo significant genetic deletion, thereby providing an  
 CC unexpectedly stable and immunogenic pox virus. They can be used to  
 CC prevent or treat tumours expressing MUC1 tumour-associated antigens  
 XX  
 SQ Sequence 26 AA;  
 Query Match 100.0%; Score 109; DB 2; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 2e-07;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GSTAPPAHGVTSAPDTRPAP 20  
 Db ||||||||||||||||  
 7 GSTAPPAHGVTSAPDTRPAP 26  
 RESULT 5  
 ADN00796  
 ID ADN00796 standard; peptide; 27 AA.  
 XX  
 AC ADN00796;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX  
 DE Human mucin 1 (MUC-1) peptide SeqID3.  
 XX  
 KW cell-specific antigen; peripheral blood mononuclear cell;  
 KW immunogenic epitope; T lymphocyte; antigen-specific activation;  
 KW tumour-specific antigen; human mucin 1; MUC-1; cytostatic;  
 KW immunosuppressive; antimicrobial; tumour; adenocarcinomas; HIV infection;  
 KW autoimmune disease; infectious disease; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004033667-A2.  
 XX  
 PD 22-APR-2004.  
 XX  
 PF 10-OCT-2003; 2003WO-US032602.  
 XX  
 PR 10-OCT-2002; 2002US-0417303P.  
 XX  
 PA (USGO ) US DEPT VETERANS AFFAIRS.  
 XX  
 PI Phillips CA;

XX WPI; 2004-340926/31.  
 DR  
 XX  
 PT Detecting and localizing a cell-specific antigen, useful in diagnosing  
 PT and treating e.g. tumors, HIV infection, autoimmune disease or infectious  
 PT disease, comprises exposing the peripheral blood mononuclear cells to an  
 PT immunogenic epitope.  
 XX  
 PS Disclosure; SEQ ID NO 3; 61pp; English.  
 XX  
 CC This invention relates to a novel method of detecting and localising a  
 CC cell-specific antigen in a mammal which comprises exposing the peripheral  
 CC blood mononuclear cells to a peptide that displays an immunogenic epitope  
 CC of the cell-specific antigen under conditions such that T lymphocytes in  
 CC the peripheral blood mononuclear cells undergo antigen-specific  
 CC activation, thus producing antigen-specific T lymphocytes that bind to  
 CC the cell-specific antigen. The cell-specific antigen is preferably a  
 CC tumour-specific antigen and the peptide displays an epitope of human  
 CC mucin 1 (MUC-1). The invention may be useful for the development of  
 CC compounds with a cytostatic, immunosuppressive or antimicrobial activity.  
 CC The method is useful in detecting and localising a cell-specific antigen  
 CC in a mammal. The method is useful in diagnosing and treating tumours,  
 CC particularly adenocarcinomas, HIV infection, autoimmune disease or  
 CC infectious disease and in monitoring response to therapy. The present  
 CC sequence is that of a human mucin 1 (MUC-1) epitope peptide which may be  
 CC used in the method of the invention.  
 XX  
 SQ Sequence 27 AA;  
 Query Match 100.0%; Score 109; DB 8; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GSTAPPAHGVTSAPDTRPAP 20  
 Db ||||||||||||||||  
 8 GSTAPPAHGVTSAPDTRPAP 27  
 RESULT 6  
 AAW03362  
 ID AAW03362 standard; peptide; 28 AA.  
 XX  
 AC AAW03362;  
 XX  
 DT 10-MAR-1997 (first entry)  
 XX  
 DE Mucin tandem repeat, ratchet library template.  
 XX  
 KW Cytotoxic T lymphocyte; CTL; epitope; mucin; ratchet library; cancer;  
 KW pharmaceutical; vaccine; treatment; prevention; disease; malignancy;  
 KW tandem repeat; template.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Region 1..20  
 FT /note= "non-MHC restricted CTL epitope"  
 XX  
 PN WO9622067-A2.  
 XX  
 PD 25-JUL-1996.  
 XX  
 PF 15-DEC-1995; 95WO-US016290.  
 XX  
 PR 27-DEC-1994; 94US-00366332.  
 XX  
 PA (UNBI-) UNITED BIOMEDICAL INC.  
 XX  
 PI Kuebler PJ, Nixon DF;  
 XX  
 DR WPI; 1996-354273/35.  
 XX  
 PT Ratchet library of peptide(s) contg. an immuno:stimulatory CTL epitope -

PT derived from longer template peptide, useful as pharmaceutical or vaccine  
 PT against infectious disease or malignancy.  
 XX Claim 9; Page 36; 60pp; English.

XX The present peptide contains a mucin tandem repeat, which elicits non-MHC  
 CC restricted cytotoxic T lymphocyte responses, and can be used as a  
 CC template in the prepn. of a ratchet library, comprising peptides contg.  
 CC at least 1 immunostimulatory CTL epitope. Basically the distribution of  
 CC amino acids at each position in the template is calculated, a ratchet  
 CC library constructed from the longer template peptide by sequentially  
 CC ratcheting it into the shorter ratchet length and the peptides  
 CC synthesised using standard solid phase methods. The library can be used  
 CC in pharmaceuticals and vaccines for the treatment, and/or prevention of  
 CC disease and malignancy associated with mucin secretion, e.g. cancer.  
 CC Several epitopes can be incorporated into the same library, rather than  
 CC using a mixt. of individually synthesised immunogenic peptides, which  
 CC helps to overcome problems of genetic diversity and MHC restrictions. The  
 CC library may also include antigenic variations and escape mutations

SQ Sequence 28 AA;

Query Match 100.0%; Score 109; DB 2; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-07;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSTAPPAHGVTSAPDTRPAP 20  
 ||||||||||||||||  
 Db 8 GSTAPPAHGVTSAPDTRPAP 27

RESULT 7  
 AAW35737  
 ID AAW35737 standard; peptide; 30 AA.

XX AC AAW35737;

DT 02-APR-1998 (first entry)

DE Mucin peptide MUC1-3.

KW MUC1; mucin; vaccine; keyhole limpet haemocyanin; KHL; cancer;  
 KW immunogenic protein; immune response.

OS Synthetic.  
 OS Mammalia.

XX PN WO9734921-A1.

PD 25-SEP-1997.

XX PF 20-MAR-1997; 97WO-US004493.

XX PR 20-MAR-1996; 96US-0013775P.

XX PA (SLOK ) SLOAN KETTERING INST CANCER RES.

XX PI Livingston PO, Zhang S;

XX WPI; 1997-480158/44.

XX Vaccine effective against cancer of the breast, prostate, colon, lung or  
 PT pancreas - comprising mucin peptide, especially MUC1, conjugated to  
 PT immunogenic protein, especially keyhole limpet haemocyanin.

PS Claim 7; Page 38; 45pp; English.

XX This mucin peptide is used in a vaccine capable of producing an immune  
 CC response which recognises a mucin. The mucin peptide is selected from  
 CC MUC1 peptide group. The vaccine comprises an amount of the mucin peptide  
 CC conjugated to an immunogenic protein effective to stimulate or enhance  
 CC immune response in the subject, together with an adjuvant and a vehicle.  
 CC The immunogenic protein is a keyhole limpet haemocyanin (KLH) or its

CC derivative. The vaccine can be used to induce an immune response in  
 CC patients suffering from a cancer of the type where the cancer cells have  
 CC mucin on their surface, e.g. breast cancer, prostate cancer, lung cancer,  
 CC colon cancer or pancreas cancer

XX SQ Sequence 30 AA;

Query Match 100.0%; Score 109; DB 2; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-07;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GSTAPPAHGVTSAPDTRPAP 20  
 ||||||||||||||||  
 Db 9 GSTAPPAHGVTSAPDTRPAP 28

RESULT 8

AAW01781

ID AAW01781 standard; peptide; 30 AA.

XX AC AAW01781;

XX DT 20-AUG-1997 (first entry)

DE Synthetic MUC1 antigen SP1-070.

XX T cell antigen epitope; Th1 specific immunomodulator; ovarian cancer;  
 KW tuberculosis; malaria; breast cancer; pancreatic cancer;  
 KW respiratory syncytial virus infection; leishmaniasis; leprosy;  
 KW candidiasis.

OS Synthetic.

XX PN WO9640066-A1.

PD 19-DEC-1996.

XX PF 07-JUN-1996; 96WO-US009951.

XX PR 07-JUN-1995; 95US-00480499.

XX PA (UYAL-) UNIV ALBERTA.

XX PI Samuel J, Kwon GS;

XX WPI; 1997-051816/05.

XX Compsn. contg. T cell antigen epitope and Th1 specific immuno:modulator -  
 PT useful for eliciting Th1 specific immune response to treat e.g. cancer,  
 PT tuberculosis, malaria, etc.

XX Example 1; Page 30; 79pp; English.

XX A novel composition is able to elicit Th1 type immune responses against  
 CC short T-cell epitope-containing peptides without the use of traditional  
 CC carrier proteins and immunoadjuvants. The composition involves: a slow  
 CC release vehicle; an immunogenically effective amount of a synthetic  
 CC peptide consisting of an 11-14 amino acid sequence containing at least  
 CC one T cell antigen epitope; and an immunogenically effective amount of a  
 CC Th1 specific immunomodulator. The present sequence is synthetic MUC1  
 CC antigen SP1-070, which was used as an example of an amino acid sequence  
 CC in the new composition and produced strong proliferation (24 to 71 fold  
 CC above background). The composition can be used to elicit a Th1 specific  
 CC immune response, preferably a protective immune response, to treat e.g.  
 CC breast, pancreatic and ovarian cancer, respiratory syncytial virus  
 CC infections, leishmaniasis, malaria, tuberculosis, leprosy and candidiasis

XX SQ Sequence 30 AA;

Query Match 100.0%; Score 109; DB 2; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-07;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSTAPPAHGVTSAPDTRPAP 20  
Db 5 GSTAPPAHGVTSAPDTRPAP 24

RESULT 9  
AAE09543  
ID AAE09543 standard; peptide; 30 AA.  
XX AC AAE09543;  
XX DT 19-NOV-2001 (first entry)  
XX DE Human mucin-1 (MUC-1) extracellular epitope #14 for CTL.  
XX KW Mucin-1; cytostatic; immunostimulant; cell mediated immune response;  
KW carcinoma; adenocarcinoma; breast cancer; dendritic cell; vaccine;  
KW gene therapy; human; MUC-1; cytotoxic T-lymphocyte; CTL.  
XX OS Homo sapiens.  
XX PN WO200157068-A1.  
XX PD 09-AUG-2001.  
XX PF 01-FEB-2001; 2001WO-AU000090.  
XX PR 01-FEB-2000; 2000AU-00005369.  
XX PR 14-JUN-2000; 2000US-00593870.  
XX PA (AUST-) AUSTIN RES INST.  
XX PI McKenzie IFC, Pietersz GA, Apostolopoulos V;  
XX DR WPI; 2001-541537/60.  
XX PT Immunostimulant peptide, used as an anti-carcinoma vaccine, comprises a  
PT an epitope of the non-VNTR, non-leader region of a mucin.  
XX PS Disclosure; Page 34; 84pp; English.  
XX CC The patent discloses peptide or polypeptides capable of eliciting an  
CC immune response, comprising an amino acid sequence corresponding to an  
CC epitope of the non-central portion of varying numbers of an amino acid  
CC motif (VNTR), non-leader region of a mucin. The peptides of the  
CC invention, fusion proteins comprising the peptide and conjugate compounds  
CC with carbohydrate polymers are used to induce a cell mediated immune  
CC response against mucin in the prevention or treatment of carcinoma,  
CC preferably adenocarcinoma, most preferably breast cancer. They are also  
CC used to pulse dendritic cell for in vivo transfer and use as a vaccine.  
CC They are also used in gene therapy. The present sequence is an  
CC extracellular peptide of mucin-1 (MUC-1) protein from human. This  
CC sequence is an epitope for cytotoxic T-lymphocytes (CTL)  
XX SQ Sequence 30 AA;

Query Match 100.0%; Score 109; DB 4; Length 30;  
Best Local Similarity 100.0%; Pred. No. 2.3e-07;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSTAPPAHGVTSAPDTRPAP 20  
Db 8 GSTAPPAHGVTSAPDTRPAP 27

RESULT 10  
AAW31695  
ID AAW31695 standard; peptide; 31 AA.  
XX AC AAW31695;  
XX DT 02-APR-1998 (first entry)  
XX FT

Query Match 100.0%; Score 109; DB 2; Length 31;  
Best Local Similarity 100.0%; Pred. No. 2.4e-07;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSTAPPAHGVTSAPDTRPAP 20  
Db 9 GSTAPPAHGVTSAPDTRPAP 28

RESULT 11  
ABG73816  
ID ABG73816 standard; peptide; 31 AA.  
XX AC ABG73816;  
XX DT 20-MAR-2003 (first entry)  
XX DE Tumour-associated antigen mucin-1 (MUC1) peptide, E31-biotin.  
XX KW Human; MUC1; mucin-1; cytostatic; antagonist; vaccine; tumour;  
KW tumour-associated mucin-1; cancer; breast carcinoma; colon carcinoma;  
KW oesophageal squamous cell carcinoma; pancreatic carcinoma;  
KW prostate carcinoma; multiple myeloma; adenocarcinoma.  
XX OS Homo sapiens.  
XX FT Key Location/Qualifiers  
FT Region 1. .8  
FT Region /label= Type\_1\_turn  
FT Region 2. .6  
FT Region /label= T\_cell\_epitope

DE Mucin peptide MUC1-3 with C-terminal cysteine.  
XX MUC1; mucin; vaccine; keyhole limpet haemocyanin; KHL; cancer;  
KW immunogenic protein; immune response; conjugate.  
XX OS Synthetic.  
OS Mammalia.  
XX PN WO9734921-A1.  
XX PD 25-SEP-1997.  
XX PF 20-MAR-1997; 97WO-US004493.  
XX PR 20-MAR-1996; 96US-0013775P.  
XX PA (SLOK ) SLOAN KETTERING INST CANCER RES.  
XX PI Livingston PO, Zhang S;  
XX DR WPI; 1997-480158/44.  
XX PT Vaccine effective against cancer of the breast, prostate, colon, lung or  
PT pancreas - comprising mucin peptide, especially MUC1, conjugated to  
PT immunogenic protein, especially keyhole limpet haemocyanin.  
XX PS Disclosure; Page 11; 45pp; English.  
XX CC This mucin peptide is used in a vaccine capable of producing an immune  
CC response which recognises a mucin. The mucin peptide is selected from  
CC MUC1 peptide group. The vaccine comprises an amount of the mucin peptide  
CC conjugated to an immunogenic protein effective to stimulate or enhance  
CC immune response in the subject, together with an adjuvant and a vehicle.  
CC A cysteine is added to the C-terminal of this peptide to facilitate the  
CC conjugation with protein carriers. The immunogenic protein is a keyhole  
CC limpet haemocyanin (KLH) or its derivative. The vaccine can be used to  
CC induce an immune response in patients suffering from a cancer of the type  
CC where the cancer cells have mucin on their surface, e.g. breast cancer,  
CC prostate cancer, lung cancer, colon cancer or pancreas cancer  
XX SQ Sequence 31 AA;

FT	Region	3. .8	/label= Alt-1 epitope
FT		/note= "Alt-1 is a TSA-specific murine monoclonal antibody. Residues 3-8 specifically claimed in claim 34"	
FT	Region	7. .12	/label= Epitope_region
FT	Region	9. .28	/label= Epitope_region
FT		/label= MUC1_extracellular_domain_core	
FT		/note= "MUC1_extracellular_domain consists of 30 to 90 tandem repeats of this sequence"	
FT	Region	11. .16	/label= Epitope_region
FT	Region	15. .20	/label= Epitope_region
FT	Region	19. .24	/label= Epitope_region
FT	Region	20. .26	/label= B_cell_epitope
FT	Region	21. .28	/label= Type_1_turn
FT	Region	22. .26	/label= T_cell_epitope
FT	Region	23. .28	/label= Alt-1 epitope
FT		/note= "Alt-1 is a TSA-specific murine monoclonal antibody. Residues 3-8 specifically claimed in claim 34"	
FT	Modified-site	31	/note= "Biotinylated"
XX			
PN	US2002132771-A1.		
XX			
PD	19-SEP-2002.		
XX			
PF	26-NOV-2001; 2001US-00994466.		
XX			
PR	18-AUG-1999; 99US-0149492P.		
PR	11-NOV-1999; 99US-0164714P.		
PR	18-AUG-2000; 2000US-00641833.		
PR	28-NOV-2000; 2000US-00724094.		
PR	21-FEB-2001; 2001US-0270456P.		
PR	21-FEB-2001; 2001US-0270471P.		
XX			
PA	(MADI/) MADIYALAKAN R.		
XX			
PI	Madiyalakan R;		
XX			
DR	WPI; 2003-155898/15.		
XX			
PT	New therapeutic compositions comprising a binding agent that binds to tumor-associated MUC1 epitope, useful for treating human tumors, e.g. breast carcinoma, prostate carcinoma or multiple myeloma.		
PT			
PT			
PS	Example 24; Page 13; 27pp; English.		
XX			
CC	The invention relates to new therapeutic compositions, which comprise a binding agent that specifically binds to an epitope of a tumour-associated mucin-1 (MUC1), are effective for treating a mammal bearing a tumour. Mice were implanted with 413BCR tumour cells 2 weeks after the start of the immunisation series (using either a conjugate of the binding agent, or a complex of the binding agent-MUC1). It was found that a humoral response was induced in mice treated with both the conjugated and complexed binding agent. A T2 cellular response to the binding agent was induced in these mice. A trend for reduction in tumour mass and size in mice treated with the conjugated or complexed binding agent was also demonstrated. The therapeutic compositions or the method is useful for treating a mammal (particularly a human) bearing a tumour, especially a tumour that expresses a tumour-associated MUC-1. In particular, the compositions are useful for treating adenocarcinomas, e.g. breast carcinoma, colon carcinoma, oesophageal squamous cell carcinoma, pancreatic carcinoma, prostate carcinoma, or multiple myeloma. The present sequence represents the mucin-1 peptide, E31-biotin		
XX			
SQ	Sequence 31 AA;		

```

Query Match      100.0%; Score 109; DB 6; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSTAPPAHGVTSPDTRPAP 20
Db 9 GSTAPPAHGVTSPDTRPAP 28
|||||

RESULT 12
AAE09541
ID AAE09541 standard; peptide; 32 AA.
XX
AC AAE09541;
XX
DT 19-NOV-2001 (first entry)
XX
DE Human mucin-1 (MUC-1) VNTR peptide #5.
XX
KW Mucin-1; cytostatic; immunostimulant; cell mediated immune response;
KW carcinoma; adenocarcinoma; breast cancer; dendritic cell; vaccine;
KW gene therapy; human; MUC-1.
XX
OS Homo sapiens.
XX
PN WO200157068-A1.
XX
PD 09-AUG-2001.
XX
PF 01-FEB-2001; 2001WO-AU0000090.
XX
PR 01-FEB-2000; 2000AU-00005369.
PR 14-JUN-2000; 2000US-00593870.
XX
PA (AUST-) AUSTIN RES INST.
XX
PI Mckenzie IFC, Pietersz GA, Apostolopoulos V;
XX
DR WPI; 2001-541537/60.
XX
PT Immunostimulant peptide, used as an anti-carcinoma vaccine, comprises a
PT an epitope of the non-VNTR, non-leader region of a mucin.
XX
PS Disclosure; Page 34; 84pp; English.
XX
CC The patent discloses peptide or polypeptides capable of eliciting an
CC immune response, comprising an amino acid sequence corresponding to an
CC epitope of the non-central portion of varying numbers of an amino acid
CC motif (VNTR), non-leader region of a mucin. The peptides of the
CC invention, fusion proteins comprising the peptide and conjugate compounds
CC with carbohydrate polymers are used to induce a cell mediated immune
CC response against mucin in the prevention or treatment of carcinoma,
CC preferably adenocarcinoma, most preferably breast cancer. They are also
CC used to pulse dendritic cell for in vivo transfer and use as a vaccine.
CC They are also used in gene therapy. The present sequence is a VNTR
CC peptide of mucin-1 (MUC-1) protein from human
XX
SQ Sequence 32 AA;

Query Match      100.0%; Score 109; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSTAPPAHGVTSPDTRPAP 20
Db 8 GSTAPPAHGVTSPDTRPAP 27
|||||

RESULT 13
AAR68002
ID AAR68002 standard; peptide; 40 AA.
XX

```



AC AAR68002;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 05-SEP-1995 (first entry)  
 XX  
 DE Mucin repeat sequence.  
 XX  
 KW Mucin; multiple tandem repeat; vaccine; pancreas cancer; breast cancer;  
 KW ovary cancer; colon cancer; HIV.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT 3. .5  
 FT /label= DTR motif  
 FT /note= "can be substituted by viral sequence, tumor  
 FT antigen or autoantigen"  
 XX  
 PN W09503825-A1.  
 XX  
 PD 09-FEB-1995.  
 XX  
 PF 29-JUL-1994; 94WO-US008477.  
 XX  
 PR 30-JUL-1993; 93US-00099354.  
 XX  
 PA (FINN/) FINN O J.  
 PA (FONT/) FONTENOT J D.  
 PA (MONT/) MONTELARO R C.  
 XX  
 PI Finn OJ, Fontenot JD, Montelaro RC;  
 XX  
 DR WPI; 1995-082033/11.  
 XX  
 PT Synthetic multiple tandem repeat mucin-1 peptides and analogues - have  
 PT native conformation in the absence of glycosylation and are linked to  
 PT epitopes; for vaccines and tests of cancer, viruses and bacteria.  
 XX  
 PS Disclosure; Page 32; 125pp; English.  
 XX  
 CC A synthetic peptide comprises at least 4 tandem repeats of the mucin  
 CC peptide given in (AAR68002). The multiple prolines of the repeat  
 CC structure are needed to maintain a rigid structure. The DTR motif,  
 CC located between the first 2 prolines in each repeat, is the target of an  
 CC anti-mucin immune response, and can be substituted by a sequence from a  
 CC virus, tumor antigen or autoantigen, for use in vaccine development.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 40 AA;  
 Query Match 100.0%; Score 109; DB 2; Length 40;  
 Best Local Similarity 100.0%; Pred. No. 3e-07;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GSTAPPAHGVTSAPDTRPAP 20  
 Db |||||  
 9 GSTAPPAHGVTSAPDTRPAP 28  
 RESULT 14  
 AAW54873  
 ID AAW54873 standard; peptide; 40 AA.  
 XX  
 AC AAW54873;  
 XX  
 DT 24-SEP-1998 (first entry)  
 XX  
 DE Carcinoma-associated antigen DF3/MUC1 tandem repeat segment.  
 DE Mucin; DF3/MUC1; cytotoxic T lymphocyte; autoimmune disease;  
 KW granuloma formation; transplant rejection.  
 XX  
 OS Homo sapiens.

XX W09817300-A1.  
 PN  
 XX 30-APR-1998.  
 PD  
 XX 24-OCT-1997; 97WO-US019784.  
 PF  
 XX 25-OCT-1996; 96US-00738262.  
 PR  
 XX (DAND ) DANA FARBER CANCER INST INC.  
 PA  
 XX Gong J, Kufe D;  
 PI  
 XX WPI; 1998-261182/23.  
 DR  
 XX Use of tandem repeat segment of mucin - as target for modulating effects  
 PT of cytotoxic T lymphocytes in the treatment of e.g. autoimmune disease,  
 PT transplant rejection or tumours.  
 XX  
 PS Disclosure; Page 28; 45pp; English.  
 XX  
 CC The tandem repeat segment of a mucin such as DF3/MUC1 can be used in an  
 CC in vivo method for decreasing or preventing the deleterious effects of  
 CC cytotoxic T lymphocytes (CTLs) in an animal. It can be used to treat  
 CC disorders characterised by activation of CTLs, such as autoimmune  
 CC diseases (e.g. diabetes, lupus and multiple sclerosis) and conditions  
 CC characterised by CTL induced granuloma formation, e.g. tuberculosis,  
 CC sarcoidosis, leprosy, Crohn's disease, hypersensitivity pneumonitis, and  
 CC primary biliary cirrhosis. The methods can also be used to treat  
 CC transplant rejection and malignant disorders of CTLs, e.g. activated T  
 CC cell leukaemia/lymphoma  
 XX  
 SQ Sequence 40 AA;  
 Query Match 100.0%; Score 109; DB 2; Length 40;  
 Best Local Similarity 100.0%; Pred. No. 3e-07;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GSTAPPAHGVTSAPDTRPAP 20  
 Db |||||  
 12 GSTAPPAHGVTSAPDTRPAP 31  
 RESULT 15  
 AAW72703  
 ID AAW72703 standard; peptide; 40 AA.  
 XX  
 AC AAW72703;  
 XX  
 DT 11-JAN-1999 (first entry)  
 XX  
 DE Human mucin peptide.  
 XX  
 KW Mucin; muc-1; human; cancer; infectious disease; vaccine; diagnosis;  
 KW multiple tandem repeat; pancreatic cancer; breast cancer; colon cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US5827666-A.  
 XX  
 PD 27-OCT-1998.  
 XX  
 PF 10-AUG-1994; 94US-00288059.  
 XX  
 PR 30-JUL-1993; 93US-00099354.  
 XX  
 PA (UYPI-) UNIV PITTSBURGH.  
 XX  
 PI Montelaro RC, Fontenot JD, Finn OJ;  
 XX  
 DR WPI; 1998-593988/50.  
 XX  
 PT Assay for cancer antibodies - using synthetic peptide comprising multiple

PT tandem repeats of muc-1.  
XX  
PS Disclosure; Col 15; 45pp; English.  
XX  
CC An assay has been developed for antibodies to pancreatic, breast or colon  
CC cancer in a sample. The assay comprises contacting the sample with a  
CC synthetic muc-1 peptide that comprises at least two 20 amino acid tandem  
CC repeats of muc-1 and is capable of attaining native conformation in the  
CC absence of glycosylation, and detecting any peptide-antibody complex  
CC formation. The assay can be used in the diagnosis of e.g. pancreatic,  
CC breast or colon cancer. The present sequence represents a human mucin  
CC peptide from the present invention  
XX  
SQ Sequence 40 AA;

Query Match 100.0%; Score 109; DB 2; Length 40;  
Best Local Similarity 100.0%; Pred. No. 3e-07;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GSTAPPAGHGVTSAPDTRPAP 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 9 GSTAPPAGHGVTSAPDTRPAP 28

Search completed: June 30, 2005, 06:42:55  
Job time : 289 secs